


## BLAST Basic Local Alignment Search Tool

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### Protein sequence(220 letters)

Results for:  

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

|cl|11706

**Description**

None

**Molecule type**

amino acid

**Query Length**

220

**Database Name**

nr

**Description**

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

**Program**

BLASTP 2.2.18+ [Citation](#)

**Reference**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference****Reference - compositional score matrix adjustment**

Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

### Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Window Size	40

### Database

Posted date May 13, 2008 5:55 PM

Number of letters 2,229,583,460  
 Number of sequences 6,530,794  
 Entrez query none

### Karlin-Altschul statistics

Params	Gapped	Ungapped
Lambda	0.322234	0.267
K	0.13584	0.041
H	0.392855	0.14

### Results Statistics

Length adjustment	129
Effective length of query	91
Effective length of database	1387111034
Effective search space	126227104094
Effective search space used	126227104094

#### Graphic Summary

##### Show Conserved Domains

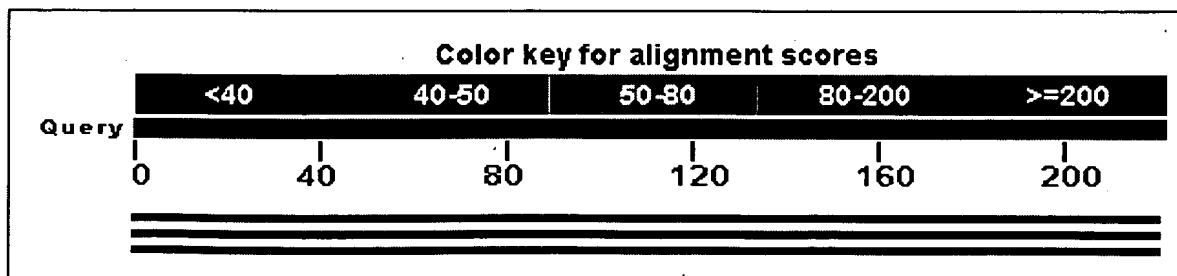
Putative conserved domains have been detected, click on the image below for detailed results.

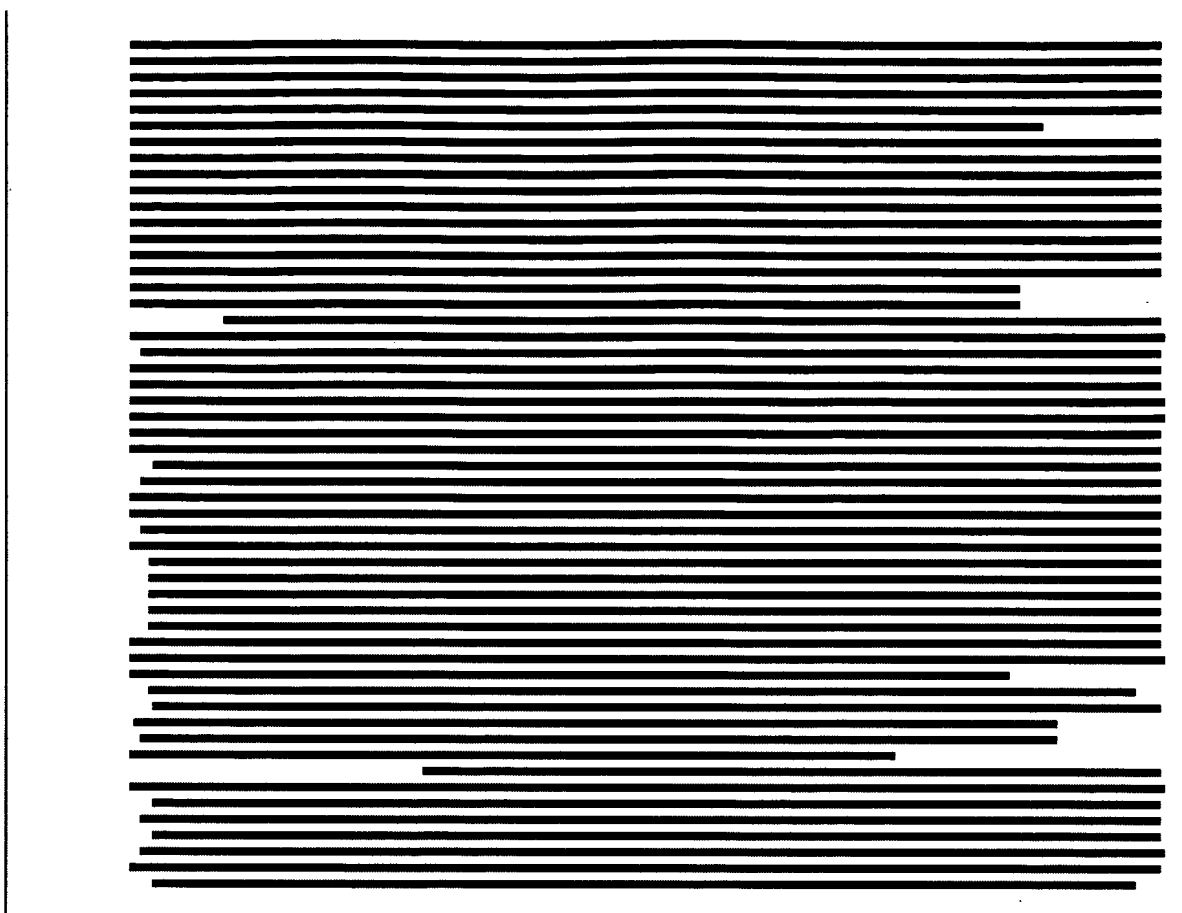


## Distribution of 101 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer

**Sequences producing significant alignments:**

(Click headers to sort columns)

<b>ABK22119.1</b>	unknown [Picea sitchensis] >gb ABK25940.1  unknown [Picea sitchensis]	406	406	99%	4e-112	
<b>NP_001059109.1</b>	Os07g0194000 [Oryza sativa (japonica cultivar-group)] >dbj BAD30158.1  synaptobrevin-like protein [Oryza sativa Japonica Group] >emb CAD70274.1  synaptobrevin 1 [Oryza sativa (japonica cultivar-group)] >dbj BAF21023.1  Os07g0194000 [Oryza sativa (japonica cultivar-group)]	389	389	99%	9e-107	<b>UG</b>
<b>NP_001051606.1</b>	Os03g0803000 [Oryza sativa (japonica cultivar-group)] >gb AAO72389.1  synaptobrevin-like protein [Oryza sativa (japonica cultivar-group)] >gb ABF99408.1  Vesicle-associated membrane protein 724, putative, expressed [Oryza sativa (japonica cultivar-group)] >dbj BAF13520.1  Os03g0803000 [Oryza sativa (japonica cultivar-group)]	387	387	99%	2e-106	<b>UG</b>
<b>CAO68808.1</b>	unnamed protein product [Vitis vinifera]	385	385	99%	8e-106	
<b>CAO63820.1</b>	unnamed protein product [Vitis vinifera]	385	385	99%	8e-106	
<b>NP_171968.1</b>	ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN) [Arabidopsis thaliana] >sp Q9MAS5 VA726_ARATH Putative vesicle-associated membrane protein 726 (AtVAMP726)	384	384	99%	2e-105	<b>UG</b>
<b>CAN81365.1</b>	hypothetical protein [Vitis vinifera] >emb CAO41974.1  unnamed protein product [Vitis vinifera]	384	384	99%	2e-105	
<b>NP_180826.2</b>	ATVAMP725 (Arabidopsis thaliana vesicle-associated membrane protein 725) >sp O48850 VA725_ARATH Vesicle-associated membrane protein 725 (AtVAMP725) >dbj BAC42934.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAP06822.1  putative synaptobrevin protein [Arabidopsis thaliana]	379	379	99%	6e-104	<b>UG</b>
<b>AAQ15287.1</b>	synptobrevin-related protein [Pyrus pyrifolia]	379	379	88%	1e-103	
<b>AAC04496.1</b>	putative synaptobrevin [Arabidopsis thaliana]	378	378	99%	1e-103	
<b>NP_171967.1</b>	VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidopsis thaliana] >sp Q92TW3 VA721_ARATH Vesicle-associated membrane protein 721 (AtVAMP721) (v-SNARE synaptobrevin 7B) (AtVAMP7B) >gb AAC98905.1  vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana] >gb AAL85003.1  Atlg04740/T1G11_1 [Arabidopsis thaliana] >gb AAM91491.1  Atlg04740/T1G11_1 [Arabidopsis thaliana] >dbj BAD42978.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43361.1  putative vesicle-associated membrane protein, synaptobrevin 7B	378	378	99%	1e-103	<b>UG</b>

[Arabidopsis thaliana] >dbj BAD43374.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43437.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43557.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43592.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43735.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD43994.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44048.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44054.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44149.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44415.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44419.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana] >dbj BAD44642.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana]					
<b>BAD43410.1</b>	putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana]	377	377	99%	3e-103
<b>AAF40460.1</b>	Strong similarity to the synaptobrevin homolog F25I18.14 gi 2924792 from A. thaliana on BAC gb AC002334. [Arabidopsis thaliana]	377	377	99%	3e-103
<b>NP_180871.1</b>	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thaliana] >sp P47192 VA722_ARATH Vesicle-associated membrane protein 722 (AtVAMP722) (Synaptobrevin-related protein 1) >gb AAL31896.1 AF419564_1 At2g33120/F25I18.14 [Arabidopsis thaliana] >gb AAC04921.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAL62414.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAL79587.1  At2g33120/F25I18.14 [Arabidopsis thaliana] >gb AAM48025.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAM64431.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAM91096.1  At2g33120/F25I18.14 [Arabidopsis thaliana]	369	369	99%	9e-101 <b>UG</b>
<b>AAA56991.1</b>	formerly called HAT24; synaptobrevin-related protein	365	365	99%	8e-100
<b>NP_001031469.1</b>	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thaliana]	360	360	99%	3e-98 <b>UG</b>
<b>ABK92923.1</b>	unknown [Populus trichocarpa] >gb ABK94486.1  unknown [Populus trichocarpa] >gb ABK95420.1  unknown [Populus trichocarpa]	357	357	99%	2e-97
<b>EAZ03095.1</b>	hypothetical protein OsI_024327 [Oryza sativa (indica cultivar-group)] >gb EAZ39005.1  hypothetical protein OsJ_022488 [Oryza sativa (japonica cultivar-group)]	357	357	99%	4e-97

EAZ28954.1	hypothetical protein OsJ_012437 [Oryza sativa 351 (japonica cultivar-group)]	351	85%	2e-95	
EAY92225.1	hypothetical protein OsI_013458 [Oryza sativa 351 (indica cultivar-group)]	351	85%	2e-95	
CAN65946.1	hypothetical protein [Vitis vinifera]	349	90%	6e-95	
ABK24294.1	unknown [Picea sitchensis]	349	100%	9e-95	
NP_001049070.1	Os03g0165800 [Oryza sativa (japonica cultivar-group)] >gb ABF94152.1  Vesicle-associated membrane protein 724, putative, expressed [Oryza sativa (japonica cultivar-group)] >dbj BAF10984.1  Os03g0165800 [Oryza sativa (japonica cultivar-group)] >gb EAY88679.1  hypothetical protein OsI_009912 [Oryza sativa (indica cultivar-group)]	346	98%	7e-94	UG
XP_001777330.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb EDQ57860.1  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	326	99%	8e-88	UG
CAO70980.1	unnamed protein product [Vitis vinifera]	325	99%	1e-87	
ABK27118.1	unknown [Picea sitchensis]	325	100%	2e-87	
ABK23325.1	unknown [Picea sitchensis]	319	100%	6e-86	
O23429	Vesicle-associated membrane protein 724 (AtVAMP724) (SYBL1-like protein) >gb AAT41760.1  At4g15780 [Arabidopsis thaliana] >gb AAT70463.1  At4g15780 [Arabidopsis thaliana]	318	99%	2e-85	
XP_001784148.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb EDQ51072.1  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	317	99%	3e-85	UG
AAV49990.1	putative synaptobrevin/VAMP [Hordeum vulgare subsp. vulgare]	303	97%	5e-81	
ABK95406.1	unknown [Populus trichocarpa]	293	98%	4e-78	
NP_190998.1	ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727) >ref NP_001078283.1  ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727) >sp Q9M376 VA727_ARATH Vesicle-associated membrane protein 727 (AtVAMP727) >emb CAB71004.1  synaptobrevin-like protein [Arabidopsis thaliana] >gb AAS47612.1  At3g54300 [Arabidopsis thaliana] >gb AAS76729.1  At3g54300 [Arabidopsis thaliana] >dbj BAF00993.1  synaptobrevin-like protein [Arabidopsis thaliana]	293	99%	4e-78	G
NP_850201.1	ATVAMP723 (Arabidopsis thaliana vesicle-associated membrane protein 723) >sp Q8VY69 VA723_ARATH Vesicle-associated membrane protein 723 (AtVAMP723) >gb AAL62392.1  putative synaptobrevin [Arabidopsis thaliana] >gb AAN15528.1  putative synaptobrevin [Arabidopsis thaliana]	289	99%	1e-76	UG
NP_001062495.1	Os08g0558600 [Oryza sativa (japonica cultivar-group)] >dbj BAD13129.1  putative	286	98%	7e-76	UG

vesicle-associated membrane protein 725  
 (AtVAMP725) [Oryza sativa Japonica Group]  
 >dbj|BAF24409.1| Os08g0558600 [Oryza sativa  
 (japonica cultivar-group)]

CAO63919.1	unnamed protein product [Vitis vinifera]	285	285	99%	2e-75	
CAJ15414.1	unnamed protein product [Triticum aestivum]	283	283	97%	5e-75	
CAJ13968.1	unnamed protein product [Aegilops tauschii]	283	283	97%	7e-75	
CAJ13552.1	unnamed protein product [Triticum turgidum]	283	283	97%	8e-75	
CAJ13539.1	unnamed protein product [Triticum aestivum]	282	282	97%	1e-74	
AAS88558.1	putative synaptobrevin [Triticum monococcum]	281	281	97%	2e-74	
NP_001030968.1	VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidopsis thaliana] >dbj BAD44122.1  putative vesicle-associated membrane protein, synaptobrevin 7B [Arabidopsis thaliana]	280	280	99%	6e-74	<b>UG</b>
XP_001779971.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb EDQ55180.1  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	278	278	100%	2e-73	<b>G</b>
NP_193313.2	ATVAMP724 (Arabidopsis thaliana vesicle-associated membrane protein 724)	275	275	85%	2e-72	<b>UG</b>
XP_001692216.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb EDP04166.1  R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	268	268	95%	2e-70	<b>UG</b>
NP_001059291.1	Os07g0249200 [Oryza sativa (japonica cultivar-group)] >dbj BAC20811.1  putative Vesicle-associated membrane protein [Oryza sativa Japonica Group] >dbj BAD30660.1  putative Vesicle-associated membrane protein [Oryza sativa Japonica Group] >dbj BAF21205.1  Os07g0249200 [Oryza sativa (japonica cultivar-group)]	266	266	97%	9e-70	<b>UG</b>
EAZ07996.1	hypothetical protein OsI_029228 [Oryza sativa (indica cultivar-group)]	263	263	89%	5e-69	
EAZ43645.1	hypothetical protein OsJ_027128 [Oryza sativa (japonica cultivar-group)]	263	263	88%	7e-69	
AAC04922.1	putative synaptobrevin [Arabidopsis thaliana]	261	261	74%	2e-68	
AAB80624.1	Strong similarity to Arabidopsis ATHSAR1 (gb M90418). ESTs gb T44122,gb N65276,gb AA041135 come from this gene. [Arabidopsis thaliana]	260	260	71%	4e-68	
XP_001764415.1	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb EDQ70682.1  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]	260	260	100%	5e-68	<b>G</b>
EAZ39281.1	hypothetical protein OsJ_022764 [Oryza sativa (japonica cultivar-group)]	253	253	97%	6e-66	
EAZ25708.1	hypothetical protein OsJ_009191 [Oryza sativa (japonica cultivar-group)]	252	252	98%	1e-65	
XP_001418265.1	predicted protein [Ostreococcus lucimarinus CCE9901] >gb ABO96558.1  predicted protein [Ostreococcus lucimarinus CCE9901]	246	246	97%	6e-64	<b>G</b>
XP_001777794.1		244	244	99%	4e-	<b>G</b>

	R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens] >gb EDQ57456.1  R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]				63	
NP_001067392.1	Os12g0639800 [Oryza sativa (japonica cultivar-group)] >gb ABA99617.1  Synaptobrevin family protein, expressed [Oryza sativa (japonica cultivar-group)] >dbj BAF30411.1  Os12g0639800 [Oryza sativa (japonica cultivar-group)]	236	236	99%	9e-61	<b>UG</b>
XP_001692208.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb EDP04158.1  R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	217	217	95%	6e-55	<b>UG</b>
EAZ03380.1	hypothetical protein OsI_024612 [Oryza sativa (indica cultivar-group)]	201	272	97%	3e-50	
XP_001692312.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb EDP04262.1  R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	186	186	95%	9e-46	<b>UG</b>
CAL53602.1	SYNAPTOBREVIN-RELATED PROTEIN 1 (IC) [Ostreococcus tauri]	182	182	83%	1e-44	
XP_001692324.1	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii] >gb EDP04274.1  R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	182	182	90%	1e-44	<b>UG</b>
NP_196676.1	ATVAMP713 (Arabidopsis thaliana vesicle-associated membrane protein 713) >sp Q9LFP1 VA713_ARATH Vesicle-associated membrane protein 713 (AtVAMP713) >emb CAB96650.1  putative protein [Arabidopsis thaliana] >gb AAM14024.1  unknown protein [Arabidopsis thaliana] >gb AAM67467.1  unknown protein [Arabidopsis thaliana]	167	167	96%	4e-40	<b>UG</b>
NP_197628.1	ATVAMP714 (Vesicle-associated membrane protein 714) [Arabidopsis thaliana] >sp Q9FMR5 VA714_ARATH Vesicle-associated membrane protein 714 (AtVAMP714) >dbj BAB08335.1  synaptobrevin-like protein [Arabidopsis thaliana]	161	161	96%	2e-38	<b>UG</b>
ABM30199.2	synaptobrevin-like protein [Brassica juncea]	161	161	96%	3e-38	
B71423	hypothetical protein - Arabidopsis thaliana >emb CAB10356.1  SYBL1 like protein [Arabidopsis thaliana] >emb CAB78620.1  SYBL1 like protein [Arabidopsis thaliana]	160	160	50%	5e-38	
NP_194942.1	VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C) [Arabidopsis thaliana] >sp O49377 VA711_ARATH Vesicle-associated membrane protein 711 (AtVAMP711) (v-SNARE synaptobrevin 7C) (AtVAMP7C) >gb AAL27509.1 AF439840_1 AT4g32150/F10N7_40 [Arabidopsis thaliana] >emb CAA16574.1  synaptobrevin-like protein [Arabidopsis thaliana] >gb AAD01748.1  vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana] >emb CAB79933.1  synaptobrevin-like protein [Arabidopsis thaliana] >gb AAM65673.1  synaptobrevin-like protein [Arabidopsis thaliana] >gb AAM78063.1  AT4g32150/F10N7_40 [Arabidopsis thaliana] >dbj BAE98551.1  vesicle-associated membrane protein 7C	156	156	96%	1e-36	<b>UG</b>



[Arabidopsis thaliana]							
CAO44255.1	unnamed protein product [Vitis vinifera]	156	156	96%	1e-36		
XP_001762112.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb EDQ73216.1  R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	156	156	86%	1e-36	<b>UG</b>	
NP_001064184.1	Os10g0154000 [Oryza sativa (japonica cultivar-group)] >gb ABB46773.2  Synaptobrevin family protein, expressed [Oryza sativa (japonica cultivar-group)] >dbj BAF26098.1  Os10g0154000 [Oryza sativa (japonica cultivar-group)]	156	156	97%	1e-36	<b>UG</b>	
XP_001778044.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb EDQ57153.1  R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	155	155	86%	2e-36	<b>UG</b>	
XP_001631076.1	predicted protein [Nematostella vectensis] >gb EDO39013.1  predicted protein [Nematostella vectensis]	155	155	96%	2e-36	<b>G</b>	
XP_001769494.1	R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens] >gb EDQ65655.1  R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]	154	154	86%	5e-36	<b>UG</b>	
ABK93000.1	unknown [Populus trichocarpa]	150	150	96%	4e-35		
XP_001698008.1	R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii] >gb EDO99593.1  R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii]	150	150	97%	6e-35	<b>UG</b>	
XP_001745842.1	predicted protein [Monosiga brevicollis MX1] >gb EDQ89266.1  predicted protein [Monosiga brevicollis MX1]	149	149	88%	1e-34	<b>G</b>	
XP_001879548.1	VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82] >gb EDR10163.1  VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82]	148	148	94%	3e-34	<b>G</b>	
EAY77730.1	hypothetical protein OsI_031689 [Oryza sativa (indica cultivar-group)]	146	146	97%	9e-34		
AAM14694.1	Putative synaptobrevin-like protein [Oryza sativa (japonica cultivar-group)] >gb EAZ15333.1  hypothetical protein OsJ_029542 [Oryza sativa (japonica cultivar-group)]	146	146	97%	9e-34		
XP_642704.1	synaptobrevin domain-containing protein [Dictyostelium discoideum AX4] >sp Q86AQ7.1 VAM7B DICDI Vesicle-associated membrane protein 7B >gb AAO51196.1  similar to Arabidopsis thaliana (Mouse-ear cress). Synaptobrevin-like protein [Dictyostelium discoideum] >gb EAL68772.1  synaptobrevin domain-containing protein [Dictyostelium discoideum AX4]	146	146	96%	1e-33	<b>UG</b>	
NP_001056946.1	Os06g0174400 [Oryza sativa (japonica cultivar-group)] >dbj BAA95814.1  putative synaptobrevin 1 [Oryza sativa Japonica Group] >dbj BAF18860.1  Os06g0174400 [Oryza sativa (japonica cultivar-group)]	145	145	96%	1e-33	<b>UG</b>	
ABK95432.1	unknown [Populus trichocarpa]	145	145	96%	2e-33		

XP_001635801.1	predicted protein [Nematostella vectensis] >gb EDO43738.1  predicted protein [Nematostella vectensis]	140	140	85%	5e-32	<b>G</b>
NP_180106.1	ATVAMP712 (Arabidopsis thaliana vesicle-associated membrane protein 712) >sp Q9SIQ9 VA712_ARATH Vesicle-associated membrane protein 712 (AtVAMP712) >gb AAD23657.1  putative synaptobrevin [Arabidopsis thaliana]	140	140	96%	5e-32	<b>UG</b>
NP_001048427.1	Os02g0803600 [Oryza sativa (japonica cultivar-group)] >dbj BAD36041.1  putative synaptobrevin 1 [Oryza sativa Japonica Group] >dbj BAF10341.1  Os02g0803600 [Oryza sativa (japonica cultivar-group)]	137	137	95%	4e-31	<b>UG</b>
NP_001086871.1	synaptobrevin-like 1 [Xenopus laevis] >gb AAH77586.1  Syb11-prov protein [Xenopus laevis]	137	137	86%	5e-31	<b>UG</b>
XP_566592.1	vesicle-associated membrane protein 712 [Cryptococcus neoformans var. neoformans JEC21] >gb AAW40773.1  vesicle-associated membrane protein 712, putative [Cryptococcus neoformans var. neoformans JEC21]	136	136	86%	8e-31	<b>G</b>
XP_778199.1	hypothetical protein CNBA1990 [Cryptococcus neoformans var. neoformans B-3501A] >gb EAL23552.1  hypothetical protein CNBA1990 [Cryptococcus neoformans var. neoformans B-3501A]	136	136	86%	1e-30	<b>G</b>
NP_001026292.1	synaptobrevin-like 1 [Gallus gallus] >sp Q5ZL74.1 VAMP7_CHICK Vesicle-associated membrane protein 7 (Synaptobrevin-like protein 1) >emb CAG31519.1  hypothetical protein [Gallus gallus]	135	135	86%	1e-30	<b>UG</b>
ABP03854.1	Longin-like [Medicago truncatula]	135	135	95%	2e-30	
NP_610524.1	CG1599 CG1599-PA [Drosophila melanogaster] >gb AAF58892.1  CG1599-PA [Drosophila melanogaster] >gb AAL49317.1  RH15778p [Drosophila melanogaster]	135	135	95%	2e-30	<b>UG</b>
NP_035645.1	vesicle-associated membrane protein 7 [Mus musculus] >sp P70280.1 VAMP7_MOUSE Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >emb CAA65509.1  synaptobrevin-like protein [Mus musculus] >emb CAB94231.1  synaptobrevin-like protein [Mus musculus] >dbj BAB22386.1  unnamed protein product [Mus musculus] >dbj BAB27667.1  unnamed protein product [Mus musculus] >gb AAH03764.1  Synaptobrevin like 1 [Mus musculus] >dbj BAC40712.1  unnamed protein product [Mus musculus] >dbj BAE38126.1  unnamed protein product [Mus musculus] >gb ABK42476.1  VAMP7 [synthetic construct] >gb EDL07809.1  synaptobrevin like 1, isoform CRA_c [Mus musculus]	134	134	86%	4e-30	<b>UG</b>
CAH69613.1	synaptobrevin 1-2 [Paramecium tetraurelia]	134	134	97%	4e-30	
XP_001439963.1	hypothetical protein GSPATT00008957001 [Paramecium tetraurelia strain d4-2] >emb CAD97455.1  synaptobrevin 1 [Paramecium tetraurelia] >emb CAK72566.1  unnamed protein	134	134	97%	4e-30	<b>G</b>

product [Paramecium tetraurelia]						
XP_795809.2	PREDICTED: similar to Syb11-prov protein [Strongylocentrotus purpuratus] >ref XP_001188931.1  PREDICTED: similar to Syb11-prov protein [Strongylocentrotus purpuratus]	134	134	96%	5e-30	<b>UG</b>
BAD96514.1	synaptobrevin-like 1 variant [Homo sapiens]	134	134	96%	6e-30	<b>G</b>
NP_005629.1	vesicle-associated membrane protein 7 [Homo sapiens] >ref XP_001100334.1  PREDICTED: synaptobrevin-like 1 isoform 3 [Macaca mulatta] >ref XP_001498248.1  PREDICTED: similar to ORF isoform 1 [Equus caballus] >sp P51809.3 VAMP7_HUMAN Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) (Tetanus-insensitive VAMP) (Ti-VAMP) >emb CAA63133.1  ORF [Homo sapiens] >emb CAB96816.1  synaptobrevin-like 1 protein [Homo sapiens] >gb AAH56141.1  Vesicle-associated membrane protein 7 [Homo sapiens] >gb EAW55882.1  synaptobrevin-like 1, isoform CRA_e [Homo sapiens] >gb EAW55883.1  synaptobrevin-like 1, isoform CRA_e [Homo sapiens]	133	133	96%	8e-30	<b>UG</b>
XP_855489.1	PREDICTED: similar to Synaptobrevin-like protein 1 [Canis familiaris]	133	133	96%	9e-30	<b>UG</b>
XP_001459953.1	hypothetical protein GSPATT00025290001 [Paramecium tetraurelia strain d4-2] >emb CAK92556.1  unnamed protein product [Paramecium tetraurelia]	133	133	97%	9e-30	<b>UG</b>
NP_445983.1	vesicle-associated membrane protein 7 [Rattus norvegicus] >sp Q9JHW5.1 VAMP7_RAT Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >gb AAF88059.1 AF281632_1 vesicle-associated membrane protein 7 [Rattus norvegicus] >gb EDL83883.1  synaptobrevin-like 1, isoform CRA_b [Rattus norvegicus]	133	133	96%	9e-30	<b>UG</b>
NP_001069770.1	vesicle-associated membrane protein 7 [Bos taurus] >sp Q17QI5.1 VAMP7_BOVIN Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) >gb AAI18342.1  Similar to Synaptobrevin-like protein 1 [Bos taurus]	133	133	96%	9e-30	<b>UG</b>
BAE99604.1	synaptobrevin-like protein [Arabidopsis thaliana]	133	133	79%	1e-29	

Alignments Select All Get selected sequences Distance tree of results

>gb|ABK22119.1| unknown [Picea sitchensis]  
 gb|ABK25940.1| unknown [Picea sitchensis]  
 Length=222

Score = 406 bits (1044), Expect = 4e-112, Method: Compositional matrix adjust.  
 Identities = 187/219 (85%), Positives = 206/219 (94%), Gaps = 0/219 (0%)

```

Query 1      MGQQSLIYAFVARGTVILA EYTEFTGNFTTIA SQCLMKLPASNNKFTYNCDGHTFN YLVE 60
                MGQQSLIY+FVARGTV+LA EYTEF GNFTTIA+QCL KLPASNNKFTYNCD HTFN YLVE
Sbjct 1      MGQQSLIYSFVARGTVVLA EYTEF KGNFTTIAAQCLQKLPASNNKFTYNCDNHTFN YLVE 60

Query 61     DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
                DGF YCVVA ES VG+Q+P+AF++RVKEDF +RYGGG+A TA NSLNR+FGSKLKEHMQY
Sbjct 61     DGFAYCVVADES VGRQVPM AFLERVKEDFKRRYGGGRADTAVGNSLNRDFGSKLKEHMQY 120

Query 121    CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
                CVDHPPEE+SKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLR QAQDF++QG
Sbjct 121    CVDHPPEEISKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRFQAQDFQKQG 180

Query 181    TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
                T +RRKMW QNMK+KLIVLGI++ALILII+LSVCHGF C
Sbjct 181    TQLRRKMWFQNMKVKLIVLGIVVALILIIIVLSVCHGFNC 219

```

>ref|NP\_001059109.1| **UG** Os07g0194000 [Oryza sativa (japonica cultivar-group)]  
 dbj|BAD30158.1| **G** synaptobrevin-like protein [Oryza sativa Japonica Group]  
 emb|CAD70274.1| **G** synaptobrevin 1 [Oryza sativa (japonica cultivar-group)]  
 dbj|BAF21023.1| **G** Os07g0194000 [Oryza sativa (japonica cultivar-group)]  
 Length=220

GENE ID: 4342638 Os07g0194000 | Os07g0194000 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 389 bits (999), Expect = 9e-107, Method: Compositional matrix adjust.  
 Identities = 212/219 (96%), Positives = 217/219 (99%), Gaps = 0/219 (0%)

```

Query 1      MGQQSLIYAFVARGTVILA EYTEFTGNFTTIA SQCLMKLPASNNKFTYNCDGHTFN YLVE 60
                MGQQSLIYAFVARGTV+LA EYTEFTGNFTTIA+QCL KLPASNNKFTYNCDGHTFN YLVE
Sbjct 1      MGQQSLIYAFVARGTVVLA EYTEFTGNFTTIAAQCLQKLPASNNKFTYNCDGHTFN YLVE 60

Query 61     DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
                DGFTYCVVAVESVG+QIPIAF+DRV KEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY
Sbjct 61     DGFTYCVVAVESVGRQIPIAFLDRV KEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120

Query 121    CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
                CVDHPPEE+SKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG
Sbjct 121    CVDHPPEEISKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180

Query 181    TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
                T VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct 181    TKVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219

```

>ref|NP\_001051606.1| **UG** Os03g0803000 [Oryza sativa (japonica cultivar-group)]  
 gb|AAO72389.1| **G** synaptobrevin-like protein [Oryza sativa (japonica cultivar-gr  
 gb|ABF99408.1| **G** Vesicle-associated membrane protein 724, putative, expressed  
 [Oryza sativa (japonica cultivar-group)]  
 dbj|BAF13520.1| **G** Os03g0803000 [Oryza sativa (japonica cultivar-group)]  
 Length=220

GENE ID: 4334472 Os03g0803000 | Os03g0803000 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 387 bits (995), Expect = 2e-106, Method: Compositional matrix adjust.  
Identities = 211/219 (96%), Positives = 216/219 (98%), Gaps = 0/219 (0%)

```

Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
Sbjct 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFN YLVE 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  DGFTYCVVAVESVG+QIQPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 121  CVDHPPEE+SKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQ G 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  T VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219

```

>emb|CAO68808.1| unnamed protein product [Vitis vinifera]  
Length=220

Score = 385 bits (990), Expect = 8e-106, Method: Compositional matrix adjust.  
Identities = 197/219 (89%), Positives = 212/219 (96%), Gaps = 0/219 (0%)

```

Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
Sbjct 2  +GQQSLIY+FVARGTVILAEYTEFTGNFT+IA+QCL KLPASNNKFTYNC DGHTFN YLVE 61

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 62  +GFTYCVVAVES G+QIQPIAF++RVK+DF KRYGGGKAATA AN LN+EFG KLKEHMQY 121

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 122  CVDHPPEE+SKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 181

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 182  T +RRKMW+QNMKIKLIVLGIIIALILII+LS+CHGFKC 220

```

>emb|CAO63820.1| unnamed protein product [Vitis vinifera]  
Length=219

Score = 385 bits (990), Expect = 8e-106, Method: Compositional matrix adjust.  
Identities = 195/219 (89%), Positives = 212/219 (96%), Gaps = 0/219 (0%)

```

Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
Sbjct 1  MGQQSLIY+FVARGTVILAE+TEF+GNFT+IA+QCL KLPA+NNKFTYNC DGHTFN YLVE 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  DG+TYCVVAVE+VG+QIQPIAF++RVKEDFTKRYGGGKAATA ANSLN+EFG KLKE MQY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 121  CVDHPPEE+SKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  T +RRKMWLQNMKIKLIVLGI+IALILII+LS+C GF C 219

```

>ref|NP\_171968.1| **UG** ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN) [Arabidops thaliana]

sp|Q9MAS5|VA726\_ARATH **G** Putative vesicle-associated membrane protein 726 (AtVAM  
Length=220

GENE ID: 839424 ATVAMP726 | ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN)  
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 384 bits (987), Expect = 2e-105, Method: Compositional matrix adjust.  
Identities = 185/219 (84%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNC DGH TFN YLVE 60
Sbjct 1  MGQOSLIY+ FVARGTVILA EYTEF GNFT++A+QCL KLP+SNNKFTYNC DGH TFN YL + 60
Query 61  DGFTYCVVAVESVGQ QIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  NGFTYCVV VIESAGRQIPMAFLERVKEDFNKRYGGGKASTAKANSLNKEFGSKLKEHMQY 120
Query 121  CVDHP EEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 121  CADHP EEISKLSKVKAQVTEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFR TQG 180
Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  T ++RK+W +NMKIKLIV GII+ALILIIILSVCHGFKC 219

```

>emb|CAN81365.1| hypothetical protein [Vitis vinifera]  
>emb|CAO41974.1| unnamed protein product [Vitis vinifera]  
Length=221

Score = 384 bits (986), Expect = 2e-105, Method: Compositional matrix adjust.  
Identities = 176/219 (80%), Positives = 200/219 (91%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNC DGH TFN YLVE 60
Sbjct 1  MGQ+SLIYAFVARGTVILA EYTEF+GNF +IA QCL KLP++NKFTYNC D HTF YL++ 60
Query 61  DGFTYCVVAVESVGQ QIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  +G+TYCVVA ES VG+Q+P+AF++R+++DF RYGG KAATA ANSLN++F SKLKEHMQY 120
Query 121  CVDHP EEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 121  CVDHP EE+SKLAKVK QVSEVKGVM MENIEKVLD RGEKIELLV DKT NL QAQDFR G 180
Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  T +RRKMWLQNMKIKLIVLGI++ALILII+LSVCHGF C 219

```

>ref|NP\_180826.2| **UG** ATVAMP725 (Arabidopsis thaliana vesicle-associated membran 725)

sp|O48850|VA725\_ARATH **G** Vesicle-associated membrane protein 725 (AtVAMP725)

dbj|BAC42934.1| **G** putative synaptobrevin [Arabidopsis thaliana]

gb|AAP06822.1| **G** putative synaptobrevin protein [Arabidopsis thaliana]  
Length=285

GENE ID: 817827 ATVAMP725 | ATVAMP725 (Arabidopsis thaliana vesicle-associated membrane protein 725) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 379 bits (974), Expect = 6e-104, Method: Compositional matrix adjust.  
Identities = 192/219 (87%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNC DGH TFN YLVE 60
Sbjct 66  MGQQ+LIY+ FVARGTVIL EYTEF GNFT +A+QCL KLP+SNNKFTYNC DGH TFN YLVE 125
Query 61  DGFTYCVVAVESVGQ QIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 126  NGFTYCVVAVESVGRQIPMAFLERVKEDFNKRYGGGKATTAQANSLNREFGSKLKEHMQY 185
Query 121  CVDHP EEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 186  CVDHP +E+SKLAKVKAQV+EVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFR QG 245
Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 246  TKIRRRKMWFENMKIKLIVLGIITLILIIILSVCGGFKC 284

```

>gb|AAQ15287.1| synptobrevin-related protein [Pyrus pyrifolia]  
Length=194

Score = 379 bits (972), Expect = 1e-103, Method: Compositional matrix adjust.  
Identities = 174/194 (89%), Positives = 190/194 (97%), Gaps = 0/194 (0%)

Query	1	MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE	60
		MGQQSLIY+FVARGTVILAEYTEFTGNFT+IASQCL KLP+NNKFTYNCDGHTFNYLV+	
Sbjct	1	MGQQSLIYSFVARGTVILAEYTEFTGNFTSIASQCLQKLPATNNKFTYNCDGHTFNYLVD	60
Query	61	DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY	120
		+GFTYCVVAVE+VG+Q+PIAF++R+KEDFT RYGGGKAATA ANSLN+EFGSKLKEHMQY	
Sbjct	61	NGFTYCVVAVEAVGRQVPIAFLEKEDFTGRYGGGKAATAVANSLNKEFGSKLKEHMQY	120
Query	121	CVDHPPEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQG	180
		CVDHPPEE+SKL+KVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQG	
Sbjct	121	CVDHPPEISKLSKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQG	180
Query	181	TNVRKMWLQNMKI	194
		T +RRKMWLQNMK+	
Sbjct	181	TQMRRKMWLQNMKL	194

>gb|AAC04496.1| putative synaptobrevin [Arabidopsis thaliana]  
Length=220

Score = 378 bits (971), Expect = 1e-103, Method: Compositional matrix adjust.  
Identities = 192/219 (87%), Positives = 207/219 (94%), Gaps = 0/219 (0%)

Query	1	MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE	60
		MGQQ+LIY+FVARGTVIL EYTEF GNFT +A+QCL KLP+SNNKFTYNCDGHTFNYLVE	
Sbjct	1	MGQQNLIYSFVARGTVILVEYTEFKNFTAVAAQCLQKLPSSNNKFTYNCDGHTFNYLVE	60
Query	61	DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY	120
		+GFTYCVVAVESVG+QIP+AF++RVKEDF KRYGGGKA TA ANSLNREFGSKLKEHMQY	
Sbjct	61	NGFTYCVVAVESVGRQIPMAFLERVKEDFNKRYGGGKATTAQANSLNREFGSKLKEHMQY	120
Query	121	CVDHPPEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQG	180
		CVDHP+E+SKLAKVKAQV+EVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFR QG	
Sbjct	121	CVDHPDEISKLAKVKAQVTEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRTQG	180
Query	181	TNVRKMWLQNMKIKLIVLGIILILILILSVCHGFKC	219
		T +RRKMW +NMKIKLIVLGIIL LILILILSVG GFKC	
Sbjct	181	TKIRKMWLFENMKIKLIVLGIILITLILILILSVCGGFKC	219

>ref|NP\_171967.1| **UG** VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabidopsis thaliana]

sp|Q9ZTW3|VA721 ARATH **G** Vesicle-associated membrane protein 721 (AtVAMP721) (v-synaptobrevin 7B) (AtVAMP7B)

gb|AAC98905.1| **G** vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

16 more sequence titles

gb|AAL85003.1| **G** At1g04740/T1G11\_1 [Arabidopsis thaliana]

gb|AAM91491.1| **G** At1g04740/T1G11\_1 [Arabidopsis thaliana]










dbj|BAD42978.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]

dbj|BAD43361.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]

dbj|BAD43374.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]

dbj|BAD43437.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]

dbj|BAD43557.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]

dbj|BAD43592.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
dbj|BAD43735.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
dbj|BAD43994.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
dbj|BAD44048.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
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dbj|BAD44149.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
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dbj|BAD44415.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
dbj|BAD44419.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
dbj|BAD44642.1|  putative vesicle-associated membrane protein, synaptobrevin 7  
[Arabidopsis thaliana]  
Length=219

GENE ID: 839419 VAMP7B | VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B)  
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 378 bits (971), Expect = 1e-103, Method: Compositional matrix adjust.  
Identities = 190/219 (86%), Positives = 208/219 (94%), Gaps = 0/219 (0%)

Query	1	MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNLYLVE	60
		M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNLYLVE	
Sbjct	1	MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNLYLVE	60
Query	61	DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY	120
		DGFTYCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY	
Sbjct	61	DGFTYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY	120
Query	121	CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQG	180
		C+DHP+E+SKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFR G	
Sbjct	121	CMDHPDEISKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRTTG	180
Query	181	TNVRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC	219
		T +RRKMWLQNMKIKLIVL IIIALILII+LSVCHGFKC	
Sbjct	181	TQMRKMWLQNMKIKLIVLAIILIIILIIIVLSVCHGFKC	219

>dbj|BAD43410.1| putative vesicle-associated membrane protein, synaptobrevin 7B  
[Arabidopsis thaliana]  
Length=219

Score = 377 bits (969), Expect = 3e-103, Method: Compositional matrix adjust.  
Identities = 189/219 (86%), Positives = 208/219 (94%), Gaps = 0/219 (0%)

Query	1	MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNLYLVE	60
		M QQSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNCDGHTFNLYLVE	
Sbjct	1	MAQQSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNCDGHTFNLYLVE	60
Query	61	DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY	120
		DGFTYCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY	
Sbjct	61	DGFTYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY	120
Query	121	CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQG	180
		C+DHP+E+SKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFR G	
Sbjct	121	CMDHPDEISKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRTTG	180
Query	181	TNVRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC	219
		+ +RRKMWLQNMKIKLIVL IIIALILII+LSVCHGFKC	
Sbjct	181	SQMRKMWLQNMKIKLIVLAIILIIILIIIVLSVCHGFKC	219

>gb|AAF40460.1|AC004809\_18 Strong similarity to the synaptobrevin homolog F25I18  
from A. thaliana on BAC-gb|AC002334. [Arabidopsis thaliana]



Length=229

Score = 377 bits (967), Expect = 3e-103, Method: Compositional matrix adjust.  
 Identities = 185/228 (81%), Positives = 207/228 (90%), Gaps = 9/228 (3%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
          MGQOSLIY+FVARGTVILAEYTEF GNFT++A+QCL KLP+SNNKFTYNC DGHTFN YL +
Sbjct 1  MGQOSLIYSFVARGTVILAEYTEFKGNFTSVAAQCLQKLPSSNNKFTYNC DGHTFN YLAD 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          +GFTYCVV +ES G+QIP+AF++RVKEDF KRYGGGKA+TA ANSLN+EFGSKLKEHMQY
Sbjct 61  NGFTYCVVVIESAGRQIPMAFLERVKEDFNKRYGGGKASTAKANSLNKEFGSKLKEHMQY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQ----- 172
          C DHPEE+SKL+KVKAQV+EVKGVM MENIEKVLDRGEKIELLV DKTENLRSQ
Sbjct 121  CADHPPEEISKLKSKVKAQVTEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQVNNNHISN 180

Query 173  -AQDFRQOGT NVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          AQDFR QGT ++RK+W +NMKIKLIV GII+ALILIIILSVCHGFKC
Sbjct 181  TAQDFRTQGT KMKRKLWFENMKIKLIVFGIIVALILIIILSVCHGFKC 228
  
```

>ref|NP\_180871.1| **UG** SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis thaliana  
 sp|P47192|VA722\_ARATH **G** Vesicle-associated membrane protein 722 (AtVAMP722) (Sy  
 protein 1)

gb|AAL31896.1|AF419564\_1 **G** At2g33120/F25I18.14 [Arabidopsis thaliana]  
 6 more sequence titles

gb|AAC04921.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
 gb|AAL62414.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
 gb|AAL79587.1| **G** At2g33120/F25I18.14 [Arabidopsis thaliana]  
 gb|AAM48025.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
 gb|AAM64431.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
 gb|AAM91096.1| **G** At2g33120/F25I18.14 [Arabidopsis thaliana]  
 Length=221

GENE ID: 817874 SAR1 | SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)  
 [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 369 bits (946), Expect = 9e-101, Method: Compositional matrix adjust.  
 Identities = 188/219 (85%), Positives = 206/219 (94%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
          M QOSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNC DGHTFN YLVE
Sbjct 1  MAQOSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNC DGHTFN YLVE 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          +GFTYCVVAV+S G+QIP+AF++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY
Sbjct 61  NGFTYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQOG 180
          C+DHP+E+SKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFR QG
Sbjct 121  CMDHPDEISKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRTQG 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          T +RRKMW QNMKIKLIVL IIIALILIIILS+C GF C
Sbjct 181  TQMRKMW FQNMKIKLIVLAIIIIALILIIILSICGGFNC 219
  
```

>gb|AAA56991.1| formerly called HAT24; synaptobrevin-related protein  
 Length=221

Score = 365 bits (938), Expect = 8e-100, Method: Compositional matrix adjust.  
 Identities = 187/219 (85%), Positives = 205/219 (93%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNNKFTYNC DGHTFN YLVE 60
          M QOSLIY+FVARGTVIL E+T+F GNFT+IA+QCL KLP+SNNKFTYNC DGHTFN YLVE
Sbjct 1  MAQOSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNC DGHTFN YLVE 60
  
```

```

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  NGFTYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQG 180
Sbjct 121  C+ HP+E+SKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFR QG 180
Sbjct 121  CMAHPDEISKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRTQG 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  T +RRKMW QNMKIKLIVL IIIIALILIIILS+C GF C 219
Sbjct 181  TQMRKMWLFQNMKIKLIVLAIIIIALILIIILSICGGFNC 219

```

>ref|NP\_001031469.1| **UG** SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) [Arabidopsis tha  
Length=229

GENE ID: 817874 SAR1 | SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)  
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 360 bits (925), Expect = 3e-98, Method: Compositional matrix adjust.  
Identities = 187/227 (82%), Positives = 206/227 (90%), Gaps = 8/227 (3%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVE 60
Sbjct 1  MAQOSLIYSFVARGTVILVEFTDFKGNFTSIAAQCLQKLPSSNNKFTYNC DGHTFNYLVE 60

Query 61  DGFT-----YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGS 112
Sbjct 61  NGFSESKYCSISYCVVAVDSAGRQIPMAFLERVKEDFNKRYGGGKAATAQANSLNKEFGS 120

Query 113  KLKEHMQYCVDPHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQ 172
Sbjct 121  KLKEHMQYCM DHPDEISKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQ 180

Query 173  AQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  AQDFRTQGTQMRKMWLFQNMKIKLIVLAIIIIALILIIILSICGGFNC 227

```

>gb|ABK92923.1| unknown [Populus trichocarpa]  
gb|ABK94486.1| unknown [Populus trichocarpa]  
gb|ABK95420.1| unknown [Populus trichocarpa]  
Length=221

Score = 357 bits (917), Expect = 2e-97, Method: Compositional matrix adjust.  
Identities = 179/219 (81%), Positives = 201/219 (91%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVE 60
Sbjct 1  MNQKSLIYAFVSRGTVILAEFTFGSGNFNSIAFQCLQKLPATNNKFTYNC DGHTFNYLAD 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  NGFTYCVVADESAGRQVPMAFLERVKDDFVSKYGGGKAATAQANGLNKEFGPKLKEHMKY 120

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQG 180
Sbjct 121  CADHPPEISKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLHSAQDFRSQG 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
Sbjct 181  TQIRKMWLQNMKVKLIVLGILIALILIIIVLSVCKGFNC 219

```

>gb|EAZ03095.1| hypothetical protein OsI\_024327 [Oryza sativa (indica cultivar-g  
gb|EAZ39005.1| hypothetical protein OsJ\_022488 [Oryza sativa (japonica cultivar  
Length=279

Score = 357 bits (915), Expect = 4e-97, Method: Compositional matrix adjust.  
Identities = 211/278 (75%), Positives = 217/278 (78%), Gaps = 59/278 (21%)

```

Query 1  MGQOSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVE 60
Sbjct 1  MGQOSLIYAFVARGTV+LAEYTEFTGNFTTIA+QCL KLPASNNKFTYNC DGHTFNYLVE 60
Sbjct 1  MGQOSLIYAFVARGTVVLAEYTEFTGNFTTIAAQCLQKLPASNNKFTYNC DGHTFNYLVE 60

```

```

Query 61  DGFT-----YCVVAVESVGQOIPIAFMDRVKEDFTKRYGGGKAATAAANSLN 107
          DGF+          YCVVAVESVG+QIPIAF+DRVKEDFTKRYGGGKAATAAANSLN
Sbjct 61  DGFSSNRIGILGIQGLAYCVVAVESVGRQIPIAFLDRVKEDFTKRYGGGKAATAAANSLN 120

Query 108  REFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE 167
          REFGSKLKEHMQYCVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE
Sbjct 121  REFGSKLKEHMQYCVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTE 180

Query 168  NLRSQ-----AQDFRQOGT 181
          NLRSQ          AQDFRQOGT
Sbjct 181  NLRSQNSGIFIQWIAMEKLLIHVSVD RMRVWSMVMKYRIMVPKVIWLTVDMAQDFRQOGT 240

Query 182  NVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct 241  KVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 278

```

>gb|EAZ28954.1| hypothetical protein OsJ\_012437 [Oryza sativa (japonica cultivar Length=346

Score = 351 bits (901), Expect = 2e-95, Method: Compositional matrix adjust.  
Identities = 176/189 (93%), Positives = 182/189 (96%), Gaps = 0/189 (0%)

```

Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
          MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE
Sbjct 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60

Query 61  DGFTYCVVAVESVGQOIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DGFTYCVVAVESVG+QIPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY
Sbjct 61  DGFTYCVVAVESVGRQIPIAFLDRVKDDFTKRYAGGKAATAAANSLNRDFGSKLKEHMQY 120

Query 121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQG 180
          CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQ G
Sbjct 121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQAG 180

Query 181  TNVRRKMWL 189
          T R+ L
Sbjct 181  TQGTRRQTL 189

```

>gb|EAY92225.1| hypothetical protein OsI\_013458 [Oryza sativa (indica cultivar-g Length=346

Score = 351 bits (900), Expect = 2e-95, Method: Compositional matrix adjust.  
Identities = 176/189 (93%), Positives = 182/189 (96%), Gaps = 0/189 (0%)

```

Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
          MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE
Sbjct 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60

Query 61  DGFTYCVVAVESVGQOIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DGFTYCVVAVESVG+QIPIAF+DRVK+DFTKRY GGKAATAAANSLNR+FGSKLKEHMQY
Sbjct 61  DGFTYCVVAVESVGRQIPIAFLDRVKDDFTKRYAGGKAATAAANSLNRDFGSKLKEHMQY 120

Query 121  CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQG 180
          CVDHPEE+SKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQ G
Sbjct 121  CVDHPEEISKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQAG 180

Query 181  TNVRRKMWL 189
          T R+ L
Sbjct 181  TQGTRRQTL 189

```

>emb|CAN65946.1| hypothetical protein [Vitis vinifera] Length=200

Score = 349 bits (896), Expect = 6e-95, Method: Compositional matrix adjust.  
Identities = 179/199 (89%), Positives = 192/199 (96%), Gaps = 0/199 (0%)

```

Query 21  YTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQOIPIA 80
          YTEFTGNFT+IA+QCL KLPASNNKFTYNCDGHTFNYLVE+GFTYCVVAVES G+QIPIA
Sbjct 2  YTEFTGNFTSIAAQCLQKLPASNNKFTYNCDGHTFNYLVENGFTYCVVAVESAGRQIPIA 61

Query 81  FMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSE 140
          F++RVK+DF KRYGGGKAATA AN LN+EPG KLKEHMQYCVDHPEE+SKLAKVKAQVSE
Sbjct 62  FLERVKDDFNKRYGGGKAATAVANGLNKEFGPKLKEHMQYCVDHPEEISKLAKVKAQVSE 121

```

Query	141	VKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGTNVRRKMWLQNMKIKLIVLG	200
		VKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGT +RRKMW+QNMKIKLIVLG	
Sbjct	122	VKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGTMRRKMWMQNMKIKLIVLG	181
Query	201	IIIALILIIILSVCHGFKC	219
		IIIALILII+LS+CHGFKC	
Sbjct	182	IIIALILIIIVLSICHGFKC	200

```
>gb|ABK24294.1| unknown [Picea sitchensis]
Length=221
```

Score = 349 bits (895), Expect = 9e-95, Method: Compositional matrix adjust.  
Identities = 155/220 (70%), Positives = 192/220 (87%), Gaps = 0/220 (0%)

Query	1	MGQQSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNC DGHFTFN YLVE	60
Sbjct	1	MG+QSLIY+ FV+RGTVILA EYTEFTGNFTT+A QCL KLPA++NKFT++C HTFN YLVE	60
Query	61	DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY	120
Sbjct	61	DGFTYCVVA ES VG+Q+PIAF++R+K++F KRY G+A A AN LN+EFG KLK+HM Y	120
Query	121	CVDHPEEVSKLAKVKAQVSEVKGVMMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG	180
Sbjct	121	C HPE+++K AK KAQV+EVKGVMM+NIEK+LDRGEKIEL+VDKTE L+ QAQDF++QG	180
Query	181	TNVR RKMWLQNMKIKLIVLGI IIALILIIILSVCHGFKCH 220	
Sbjct	181	T +RRKMW +NMK+KLI L ++ +IL+I +S+C GFKCH	
Query	241	TOIRRKMWFRNMKVKLICLSFLLFVILMIWISLCRGFKCH 220	
Sbjct	241	T OIRRKMWFRNMKVKLICLSFLLFVILMIWISLCRGFKCH 220	

```
>ref|NP_001049070.1| UG Os03g0165800 [Oryza sativa (japonica cultivar-group)]
  gb|ABF94152.1| G Vesicle-associated membrane protein 724, putative, expressed
[Oryza sativa (japonica cultivar-group)]
  dbj|BAF10984.1| G Os03g0165800 [Oryza sativa (japonica cultivar-group)]
  gb|EAY88679.1| hypothetical protein OsI_009912 [Oryza sativa (indica cultivar-g
Length=223
```

GENE ID: 4331733 Os03g0165800 | Os03g0165800 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 346 bits (887), Expect = 7e-94, Method: Compositional matrix adjust.  
Identities = 152/217 (70%), Positives = 188/217 (86%), Gaps = 0/217 (0%)

Query	3	QQSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNKKFTYNCDGHTFNYLVEDG + +L+Y+FVARG V+LA++ E +GNF ++A+QCL KLP++NN+ +YNCDGHTFNY V DG	62
Sbjct	6	RTTLVYSFVARGAVVLADHAEVSGNFASVAAQCLQKLPSTNNRHSYNCDGHTFNYHVHDG	65
Query	63	FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV FTYCVVA ES G+Q+P+ F++RVKEDF+K+Y GGKA A ANSL RE+G KLKEHM+YC	122
Sbjct	66	FTYCVVATESAGRQLPVGFIERVKEDFSKKYSGGKAKNATANSLKREYGPKLKEHMKYCD	125
Query	123	DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOQGTN HPEE+ KLAKVKAQV+EVKGVMM+NIEKVLDRGEKIELLVDKTE+LRSQAQDFR+ GT	182
Sbjct	126	AHPEEIDKLAKVKAQVTEVKGVMQNIEKVLDRGEKIELLVDKTEDLRSQAQDFRKAGTK	185
Query	183	VRRKMWLQNMKIKLIVLGIILIIILSVCHGFKC 219 +RRKMW +NMK+KLIV GI++ALIL+IIL+VC C	
Sbjct	186	IRRKMMWENNMKMLIVFGIVVALILVLIILTVCRDLNC 222	

```
>ref|XP_001777330.1| UG R-SNARE, VAMP72-family [Physcomitrella patens subsp. pa  
gb|EDQ57860.1| G R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
Length=222
```

Score = 326 bits (835), Expect = 8e-88, Method: Compositional matrix adjust.  
Identities = 157/219 (71%), Positives = 191/219 (87%), Gaps = 0/219 (0%)

Query 1 MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNKFTYNC DGHTFNYLVE 60  
MG QSLIY+ FVARG+ +LAEYT F+GNF+TIA QCL KLP +NNKFTY CD HTFNYLVE

```

Sbjct 1  MGTQSLIYSFVARGSTVLAEYTAFGSGNFSTIAVQCLQKLPPNNNKFTYTCDRHTFNLYVE 60
Query 61  DGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          +G+TY VVA E  G+QIP AF++RVKEDF +RY GGKA +A ANSL++EFG KLK+HMQY
Sbjct 61  EGYTYLVVADEEFGRQIPFAFLERVKEDFKRRYAGGKADSAIANSLDKEFGPKLKDHHMQY 120
Query 121 CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG 180
          CVDHP+E++K++K+K+QV+EVKG+MM+NIEKVLDRGEKIELLVDKTENLR QA +F++QG
Sbjct 121 CVDHPDEMKNISKIKSQVAEVKGIMMDNIEKVLDRGEKIELLVDKTENLRFQADNFQRQG 180
Query 181 TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          +RRKMW QNMK+KLIVL III +I+II LS+C GF C
Sbjct 181 KQLRRKMWFQNMKVKLIVLAIIVIIIIIIWLSICRGFTC 219

```

>emb|CAO70980.1| unnamed protein product [Vitis vinifera]  
Length=221

Score = 325 bits (833), Expect = 1e-87, Method: Compositional matrix adjust.  
Identities = 151/219 (68%), Positives = 187/219 (85%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILAELYTEFTGNFTTASQCLMKLPASNNKFTYNCDCGHTFNLYVE 60
          M Q+S IY+FVARGT++LAELYTEFTGNF IA+QCL +LP++NNKFTYNCDC HTFN+LVE
Sbjct 1  MSQESFIYSFVARGTMVLAELYTEFTGNFPAIATQCLQRLPSANNKFTYNCDCGHTFNFLVE 60
Query 61  DGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DG+ YCVVA ESVA+Q+ IAF++R+K DF KRYGGGKA TA A SLN++FG +KEHMQY
Sbjct 61  DGYAYCVVAKESVGKQVSIAPFLERMKADFKKRYGGGKADTATAKSLNKDFGPIMKEHMQY 120
Query 121 CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG 180
          +DH EE+ KL KVKAQVSEVK +M+ENI+K L+RGE + +L DKTE+LRSQAQ F++QG
Sbjct 121 IIDHAEEIEKLLKVKAQVSEVKSIMLENIDKTLENGENLTILADKTEDLRSQAQQFQKQG 180
Query 181 TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          + VRRKMW QNMKIKL+VLGI++ L L+I +S+CHGF C
Sbjct 181 SQVRRKMWFQNMKIKLVLVGLIILALVIWVSICHGFNC 219

```

>gb|ABK27118.1| unknown [Picea sitchensis]  
Length=219

Score = 325 bits (832), Expect = 2e-87, Method: Compositional matrix adjust.  
Identities = 144/220 (65%), Positives = 189/220 (85%), Gaps = 1/220 (0%)

```

Query 1  MGQOSLIYAFVARGTVILAELYTEFTGNFTTASQCLMKLPASNNKFTYNCDCGHTFNLYVE 60
          M QOSLIY+FVARG ++LAE+T F+GNF+ IA QCL KLP+++NKFTY CD HTFNLYLV+
Sbjct 1  MAQOSLIYSFVARGNIVLAEHTSFSGNFSIIAVQCLQKLPSNSNKFTYTCNHTFNLYVD 60
Query 61  DGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DGF + VV+ E+ G+Q+P F++RVKEDF +RYGG +A T+ A+SL++++G L++HMQY
Sbjct 61  DGFVFLVVSDEAAGRQVPFLFLERVKEDFKRRYGG-RAETSMASLDKDYGPILRDHMQY 119
Query 121 CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQG 180
          C+DHPEE+SK +K+KAQVSEVKG+MM+NIEKVLDRGEKIELLVDKTE L+ QA +F++QG
Sbjct 120 CMDHPEELSKFSKIKAQVSEVKGIMMDNIEKVLDRGEKIELLVDKTEGLQFQADNFQRQG 179
Query 181 TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH 220
          +RRKMWLQN+K K+IVLG ++++ILII LSV C GF C+
Sbjct 180 RQLRRKMWLQNLKFKIIVLGTVLSIILIIWLSVCKGFSCN 219

```

>gb|ABK23325.1| unknown [Picea sitchensis]  
Length=235

Score = 319 bits (818), Expect = 6e-86, Method: Compositional matrix adjust.  
Identities = 148/236 (62%), Positives = 189/236 (80%), Gaps = 17/236 (7%)

```

Query 1  MGQOSLIYAFVARGTVILAELYTEFTGNFTTASQCLMKLPASNNKFTYNCDCGHTFNLYVE 60
          M QOSLIY+FVARG ++LAE+T F+GNF+ IA QCL KLP+++NKFTY CD HTFNLYLV+
Sbjct 1  MAQOSLIYSFVARGNIVLAEHTSFSGNFSIIAVQCLQKLPSNSNKFTYTCNHTFNLYVD 60
Query 61  DGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLN----- 107
          DGF + VVA E+ G+Q+P F++RVKEDF +RYGG +A T+ A+SL+
Sbjct 61  DGFVFLVVADEAAGRQVPFLFLERVKEDFKRRYGG-RAETSMASLDKDYGYEEKFSVAY 119
Query 108 ---REFGSKLKEHMQYCVDPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLV 164

```

```

      REFG L++HMQYC+DHPEE+SK +K+KAQVSEVKG+MM+NIEKVLDRGEKIELLV
Sbjct 120 NLDREFGPILRDHMQYCMDHPEELSKFSKIKAQVSEVKGIMMDNIEKVLDRGEKIELLV 179
Query 165 KTENLRSQAQDFRQQGTNVRKMWLQNMKIKLIVLGIILIIILSVCHGFKCH 220
      KTE L+ QA +F++QG +RRKMWLQN+K K+IVLG ++++ILII LSVC GF C+
Sbjct 180 KTEGLQFQADNFQRQGRQLRRKMWLQNLKFKIIVLGTVLSIILIIWLSVCKGFSCN 235

```

>sp|O23429|VA724\_ARATH Vesicle-associated membrane protein 724 (AtVAMP724) (SYBL protein)

```

gb|AAT41760.1| At4g15780 [Arabidopsis thaliana]
gb|AAT70463.1| At4g15780 [Arabidopsis thaliana]
Length=222

```

Score = 318 bits (815), Expect = 2e-85, Method: Compositional matrix adjust.  
Identities = 156/220 (70%), Positives = 190/220 (86%), Gaps = 1/220 (0%)

```

Query 1  MGQOSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNN-KFTYNCDGHTFNYLV 59
Sbjct 1  MGQ+S IY+FVARGT+ILA EYTEFTGNF +IA+QCL KLP+S+N KFTYNCD HTFN+LV 60
      MGQESFIYSFVARGTMILA EYTEFTGNFP SIAAQCLQKLPSSSNSKFTYNCDHHTFNF LV
Query 60  EDGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQ 119
Sbjct 61  EDG+ YCVVA +S+ +QI IAF++RVK DF KRYGGGKA+TA A SLN+EFG +KEHM 120
      EDGYAYCVVAKDSLKQISIAFLERVKADF KRYGGGKASTAI AKSLNKEFGPVMKEHMN
Query 120 YCVDHPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQQ 179
Sbjct 121 YIVDHAEIEKLIKVKAQVSEVKSIMLENIDKAIDRGENLTVLTDKTENLRSQAQ EYKKQ 180
      Y VDH EE+ KL KVKAQVSEV K+M+ENI+K +DRGE + +L DKTENLRSQAQ++Q
Query 180 GTNVRKMWLQNMKIKLIVLGIILIIILSVCHGFKC 219
Sbjct 181 GTVRRK+W QNMKIKL+VLGI++ L+LII +SVCHGF C 220
      GTQVRRKLWYQNMKIKLVVLGILLLLVLIIWISVCHGFNC

```

>ref|XP\_001784148.1| **UG** R-SNARE, VAMP72-family [Physcomitrella patens subsp. pa  
gb|EDQ51072.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
Length=220

Score = 317 bits (813), Expect = 3e-85, Method: Compositional matrix adjust.  
Identities = 156/219 (71%), Positives = 190/219 (86%), Gaps = 0/219 (0%)

```

Query 1  MGQOSLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
Sbjct 1  MG QSLIY+FVARG +LA EYT F+GNF+TIA QCL KLP +NNKFTY CD HTFNYLVE 60
      MGTQSLIYSFVARGPTVLA EYTA FSGNFSTIAVQCLQKLPNNNNKFTYTCDRHTFNYLVE
Query 61  DGFTYCVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
Sbjct 61  +G+TY VVA E G+QIP AF++RVKEDF +RY GGKA +A A+SL++EFG KLK+HMQY 120
      EGYTYLVVADEEFGRQIPFAFLERVKEDFKRRYAGGKADSAIAHSLDKEFGPKLKD HMQY
Query 121 CVDHPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQQG 180
Sbjct 121 CVDHP+E++K++K+K+QV+EVKG+MM+NIEKVLDRGEKIELLV DKTENLR QA +F++QG 180
      CVDHPDEM NKISKIKSQVAEVKGIMMDNIEKVLDRGEKIELLV DKTENLRFQADNFQRQG
Query 181 TNVRKMWLQNMKIKLIVLGIILIIILSVCHGFKC 219
Sbjct 181 +RRKMW QNMK+KLIVL III +I+II LS+C GF C 219
      RQLRRKMWFQNMKVKLIVLAI IIVV I I I I I WLSICRGFTC

```

>gb|AAV49990.1| putative synaptobrevin/VAMP [Hordeum vulgare subsp. vulgare]  
Length=215

Score = 303 bits (777), Expect = 5e-81, Method: Compositional matrix adjust.  
Identities = 140/214 (65%), Positives = 181/214 (84%), Gaps = 0/214 (0%)

```

Query 6  LIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNCDGHTFNYLV EDGFTY 65
Sbjct 1  +IYA VARGTV++AE+T +TGNF IA QCL KLPA +++F YNCDGHTF +L+ G+ Y 60
      MIYAMVARGTVVVAEHTAYTGNFRDIAGQCLHKLPAGDSRFAYNCDGHTFTFLHQGYAY
Query 66  CVVAVESVGQOPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV DHP 125
Sbjct 61  CVVA ES G+++P+AF++R+KEDF +RY GGKAATA ANSL ++FG +LKE M+YC+DHP 120
      CVVATESAGREVPLAFLERIKEDFNRRYAGGKAATATANS LTKDFGPRLKEQMKYCMDHP
Query 126 EEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQQGTNVR 185
      EEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L A DFR +GT +RR

```

```

Sbjct 121 EEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHALDFRTEGTRIRR 180
Query 186 KMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
      +MW QNMKIKLIV+GI++ALILII+LS+CH C
Sbjct 181 RMWYQNMKIKLIVVGIVVALILIIIVLSICHKKDC 214

```

>gb|ABK95406.1| unknown [Populus trichocarpa]  
Length=238

Score = 293 bits (751), Expect = 4e-78, Method: Compositional matrix adjust.  
Identities = 133/235 (56%), Positives = 184/235 (78%), Gaps = 18/235 (7%)

```

Query 3 QQSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNKFTYNC DGHTFNLYLVEDG 62
      Q+ LIY+FVA+G V+LAE+T ++GNF+TIA QCL KLP++++K+TY+ DGHTFN+L+++G
Sbjct 4 QKGLIYSFVAKGNVLA EHTSYSGNFSTIAVQCLQKLP SNSSKYTYSSDGH TFNFLIDNG 63

Query 63 FTYCVVAVESVGGQIPIAFMDRVKEDFTKRYGGGKAATA-----AAN 104
      F+ VVA ES VG+ + F++RVK+DF +RYG A A
Sbjct 64 FVFLVVADES VGRGVSVFVLERVKDDFNQRYGASIKNEAHPLADDDDDDDLFEDRFSIAY 123

Query 105 SLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLVD 164
      +L+REFG +LKEHMQYCV+HPEE+SKL+K+KAQ++EVKG+MM+NI+KVLDRGE+IELLVD
Sbjct 124 NLDREFGPRLKEHMQYCVNHPEEISKLSKLKAQITEVKGIMMDNIDKVLDRGERIELLVD 183

Query 165 K TENLR SQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
      KT+NL QA F++QG +RRKMWLQ+K+KL++ G ++ALI+I+ +SVC GFKC
Sbjct 184 KTDNLSFQADSFQRQGRELRRKMWLQNLKVKLVLGGTVLALIVIVWISVCGGFKC 238

```

>ref|NP\_190998.1| **G** ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane 727)

ref|NP\_001078283.1| **UG** ATVAMP727 (Arabidopsis thaliana vesicle-associated memb 727)

sp|Q9M376|VA727 ARATH **G** Vesicle-associated membrane protein,727 (AtVAMP727)

emb|CAB71004.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

gb|AAS47612.1| **G** At3g54300 [Arabidopsis thaliana]

gb|AAS76729.1| **G** At3g54300 [Arabidopsis thaliana]

dbj|BAF00993.1| **G** synaptobrevin -like protein [Arabidopsis thaliana]  
Length=240

GENE ID: 824597 ATVAMP727 | ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 293 bits (751), Expect = 4e-78, Method: Compositional matrix adjust.  
Identities = 137/239 (57%), Positives = 181/239 (75%), Gaps = 21/239 (8%)

```

Query 1 MGQQSLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNKFTYNC DGHTFNLYLVE 60
      M Q+ LIY+FVA+GTV+LAE+T ++GNF+TIA QCL KLP +++K+TY+CDGHTFN+LV+
Sbjct 1 MSQKGLIYSFVAKGTVVLA EHTPTYSNGNFSTIAVQCLQKLP TNSSKYTYSCDGH TFNFLVD 60

Query 61 DGFTYCVVAVESVGGQIPIAFMDRVKEDFTKRYGG-----GKAAT 100
      +GF+ VVA ES G+ +P F++RVKEDF KRY G +
Sbjct 61 NGFVFLVVADESTGRSVPFVFLERVKEDFKKRYEASIKNDERHPLADEDEDDDDLFGDRFS 120

Query 101 AAANSLNREFGSKLKEHMQYCVDHPEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIE 160
      A N L+REFG LKEHMQYC+ HPEE+SKL+K+KAQ++EVKG+MM+NIEKVLD RGEKIE
Sbjct 121 VAYN-LDREFGPILKEHMQYCM SHPEEMSKLSKLKAQITEVKGIMMDNIEKVLD RGEKIE 179

Query 161 LLVDKTENLR SQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
      LLVDKTENL+ QA F++QG +RRKMWLQ++++KL+V G + + ILI+ + C GFKC
Sbjct 180 LLVDKTENLQFQADSFQRQGRQLRRKMWLQSLQMKLMVAGAVFSFILIVWVACGGGFKC 238

```

>ref|NP\_850201.1| **UG** ATVAMP723 (Arabidopsis thaliana vesicle-associated membran 723)

sp|Q8VY69|VA723 ARATH **G** Vesicle-associated membrane protein 723 (AtVAMP723)

gb|AAL62392.1| **G** putative synaptobrevin [Arabidopsis thaliana]

gb|AAN15528.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
Length=217

GENE ID: 817873 ATVAMP723 | ATVAMP723 (Arabidopsis thaliana vesicle-associated membrane protein 723) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 289 bits (739), Expect = 1e-76, Method: Compositional matrix adjust.  
Identities = 155/219 (70%), Positives = 179/219 (81%), Gaps = 4/219 (1%)

```
Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVE 60
          M QQSL Y+F+ARGTVIL E+T+F GNFT++A+Q L LP+SNNKFTYNC DGHTFN LVE
Sbjct 1  MAQQSLFYFIARGTVILVEFTDFKGNFTSVAAQYLENLPSSNNKFTYNC DGHTFNDLVE 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          +GFTYCVVAV+S G++IP+AF++RVKEDF KRYGG KAAT ANSLN+EFGS LKEHMQY
Sbjct 61  NGFTYCVVAVDSAGREIPMAFLERVKEDFYKRYGGEKAATDQANSLNKEFGSNLKEHMQY 120

Query 121 CVDHPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLV DKTENLR SQAQDFRQQG 180
          C+DHP+E+S LAK KAQVSEVK +MMENIEKVL RG E+L SQ Q F +
Sbjct 121 CMDHPDEISNLAKAKAQVSEVKSMMENIEKVLARGVICEMLGSS----ESQPQAFYIKR 176

Query 181 TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          T ++RK W QNMKIKLIVL IIALILIIILSV C GF C
Sbjct 177 TQMKRKKWFQNMKIKLIVLAIILIIILSVCGGFNC 215
```

>ref|NP\_001062495.1| **UG** Os08g0558600 [Oryza sativa (japonica cultivar-group)]  
dbj|BAD13129.1| **G** putative vesicle-associated membrane protein 725 (AtVAMP725)  
[Oryza sativa Japonica Group]  
dbj|BAF24409.1| **G** Os08g0558600 [Oryza sativa (japonica cultivar-group)]  
Length=241

GENE ID: 4346309 Os08g0558600 | Os08g0558600 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 286 bits (732), Expect = 7e-76, Method: Compositional matrix adjust.  
Identities = 133/237 (56%), Positives = 177/237 (74%), Gaps = 20/237 (8%)

```
Query 3  QQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVEDG 62
          +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP + +K TY+CDGHTFN+LV+ G
Sbjct 5  KQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPNTSKSTYSCDGHTFNFLVDRG 64

Query 63  FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGG-----KAATAA 102
          F + VVA E+VG+ +P F+DRVKEF +RYG + +
Sbjct 65  FVFLVVADEAVGRSVPFVFLDRVKEFDMQRYGSSIDEEGQHPLADDADDDDFLLED RFSI 124

Query 103 ANSLNREFGSKLKEHMQYCVDPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELL 162
          A +L+REFG +LK+HM YC++HPEE+SKL+KVKA ++EVKG+MM+NIEK+L+RGEKIELL
Sbjct 125 AYNLDREFGPRLKDHMLYCINHPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIELL 184

Query 163 VDKTENLR SQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          V KTE L+SQA F + G +RRKMWLQN++ KL+V G + ALIL + L +C GFKC
Sbjct 185 VGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLMVGGAVAALILFLWLIICGGFKC 241
```

>emb|CAO63919.1| unnamed protein product [Vitis vinifera]  
Length=239

Score = 285 bits (728), Expect = 2e-75, Method: Compositional matrix adjust.  
Identities = 138/239 (57%), Positives = 185/239 (77%), Gaps = 20/239 (8%)

```
Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVE 60
          M Q+ LIY+FVA+GTV+LAE+T F+GNF+TIA QCL KLP++++K+TY+CDGHTFN+L++
Sbjct 1  MSQKGLIYSFVAKGTVVLAEHTSFSGNFSTIAVQCLQKLPSSSKYTYSCDGHTFNFLID 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAA----- 102
          GF + VVA ES G+ P F++RVK+DF +RYGG +
Sbjct 61  SGFVFLVVADESAGRGAPFVFLERVKDDFKQRYGGSIRSDGPHPLADED DDDDDLFEDRF 120

Query 103 --ANSLNREFGSKLKEHMQYCVDPPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIE 160
          A +L+REFG KLKEHMQY++HPEE+SKL+K+KAQ++EVKG+MM+NIEKVLDRGE+IE
Sbjct 121 SIAYNLDREFGPRLKDHMLYCINHPEEISKLSKLKAQITEVKGIMMDNIEKVLDRGERIE 180
```



```

Query 161 LLVDKTENLRSAQDFRQOGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          LLVDKTENL+ QA F++QG +RRKMWLQN+++KL+V GI++ LI+I+ L C GFKC
Sbjct 181 LLVDKTENLQFQADSFQRQGRQLRRKMWLQNLRLKLMVGGIVLVLIILWLIACKGFKC 239

```

>emb|CAJ15414.1| unnamed protein product [Triticum aestivum]  
Length=231

Score = 283 bits (724), Expect = 5e-75, Method: Compositional matrix adjust.  
Identities = 139/215 (64%), Positives = 183/215 (85%), Gaps = 0/215 (0%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
        ++IYA VARGT+++AE+T +TGNF IA+QCL KLPA +++FTY CDGHTF +L+ G+
Sbjct 16 TMIYAMVARGTLVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHTFTFLHQQGYA 75

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
        YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL+++FG +LKE MQYC+DH
Sbjct 76 YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLSKDFGPRLKEQMQYCMDH 135

Query 125 PEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQOGTNVR 184
        PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L A DFR +GT +R
Sbjct 136 PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHAMDFRTEGTRLR 195

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
        R+MW QNMKIKLIV GI++A+ILII+LS+CH C
Sbjct 196 RRMWYQNMKIKLIVAGIVVAIILIIIVLSICHRDHC 230

```

>emb|CAJ13968.1| unnamed protein product [Aegilops tauschii]  
Length=231

Score = 283 bits (723), Expect = 7e-75, Method: Compositional matrix adjust.  
Identities = 139/215 (64%), Positives = 182/215 (84%), Gaps = 0/215 (0%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
        ++IYA VARGT+++AE+T +TGNF IA+QCL KLPA +++FTY CDGHTF +L+ G+
Sbjct 16 TMIYAMVARGTLVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHTFTFLHQQGYA 75

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
        YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LKE MQYC+DH
Sbjct 76 YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANS�TKDFGPRLKEQMQYCMDH 135

Query 125 PEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQOGTNVR 184
        PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+I+ LV +TE L A DFR +GT +R
Sbjct 136 PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIDGLVTRTEQLHDHAMDFRTEGTRLR 195

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
        R+MW QNMKIKLIV GI++A+ILII+LS+CH C
Sbjct 196 RRMWYQNMKIKLIVAGIVVAIILIIIVLSICHRDHC 230

```

>emb|CAJ13552.1| unnamed protein product [Triticum turgidum]  
Length=232

Score = 283 bits (723), Expect = 8e-75, Method: Compositional matrix adjust.  
Identities = 139/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
        ++IYA VARGT+++AE+T +TGNF IA+QCL KLPA +++FTY CDGH F +L+ G+
Sbjct 16 TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFITFLHQQGYA 75

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
        YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LKE MQYC+DH
Sbjct 76 YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANS�TKDFGPRLKEQMQYCMDH 135

Query 125 PEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQOGTNVR 184
        PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV +TE L A DFR +GT +R
Sbjct 136 PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR 195

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
        R+MW QNMKIKLIV GI++A+ILII+LS+CH C
Sbjct 196 RRMWYQNMKIKLIVAGIVVAIILIIIVLSICHRDHC 230

```

>emb|CAJ13539.1| unnamed protein product [Triticum aestivum]  
Length=232

Score = 282 bits (722), Expect = 1e-74, Method: Compositional matrix adjust.  
Identities = 139/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

```

Query 5    SLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          ++IYA VARGT+++AE+T +TGNF IA+QCL KLPA +++FTY CDGH F +L+ G+
Sbjct 16   TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFTFLHQGYA 75

Query 65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LKE MQYC+DH
Sbjct 76   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKEQM QYCMDH 135

Query 125  PEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTNVR 184
          PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV +TE L A DFR +GT +R
Sbjct 136  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR 195

Query 185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          R+MW QNMKIKLIV GI++A+ILII+LS+CH C
Sbjct 196  RRMWYQNMKIKLIVAGIVVAIILIIIVLSICHRDHC 230

```

>gb|AAS88558.1| putative synaptobrevin [Triticum monococcum]  
Length=218

Score = 281 bits (719), Expect = 2e-74, Method: Compositional matrix adjust.  
Identities = 138/215 (64%), Positives = 181/215 (84%), Gaps = 0/215 (0%)

```

Query 5    SLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          ++IYA VARGT+++AE+T +TGNF IA+QCL KLPA +++FTY CDGH F +L+ G+
Sbjct 2    TMIYAMVARGTMVVAEHTAYTGNFRDIAAQCLHKLPAGDSRFTYTCDGHAFTFLHQGYA 61

Query 65   YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          YCVVA ES G+++P+AF++R+KE+F KRY GGKAATA ANSL ++FG +LK+ MQYC+DH
Sbjct 62   YCVVATESAGREVPLAFLERIKEEFNKRYAGGKAATATANSLTKDFGPRLKDQM QYCMDH 121

Query 125  PEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTNVR 184
          PEEVS+L+KV+AQVSEVKG+MMENI+KV+DRGE+IE LV +TE L A DFR +GT +R
Sbjct 122  PEEVSRLSKVQAQVSEVKGIMMENIDKVIDRGEQIEGLVTRTEQLHDHALDFRTEGTRIR 181

Query 185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          R+MW QNMKIKLIV GI++A+ILII+LS+CH C
Sbjct 182  RRMWYQNMKIKLIVAGIVVAIILIIIVLSICHRDHC 216

```

>ref|NP\_001030968.1| **UG** VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B) [Arabid thaliana]

dbj|BAD44122.1| **G** putative vesicle-associated membrane protein, synaptobrevin 7 [Arabidopsis thaliana]  
Length=181

GENE ID: 839419 VAMP7B | VAMP7B (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7B)  
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 280 bits (716), Expect = 6e-74, Method: Compositional matrix adjust.  
Identities = 155/219 (70%), Positives = 170/219 (77%), Gaps = 38/219 (17%)

```

Query 1    MGQQSLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
          M QQSLIY+FVARGTVIL E+T+F
Sbjct 1    MAQQSLIYSFVARGTVILVEFTDFKA----- 26

Query 61   DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          YCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EF GSKLKEHMQY
Sbjct 27   ----YCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQY 82

Query 121  CVDHPPEEVSKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
          C+DHP+E+SKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFR G
Sbjct 83   CMDHPDEISKLAKVKAQVSEVKGVM MENIEKVLD RGEKIELLV DKTENLRSQAQDFRTTG 142

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          T +RRKMWLQNMKIKLIVL IIIIALILII+LSVCHGFKC
Sbjct 143  TQMRRKMWLQNMKIKLIVLAIIIIALILIIIVLSVCHGFKC 181

```

>ref|XP\_001779971.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. pate  
gb|EDQ55180.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
Length=239

Score = 278 bits (711), Expect = 2e-73, Method: Compositional matrix adjust.  
Identities = 132/220 (60%), Positives = 174/220 (79%), Gaps = 0/220 (0%)

```

Query   1      MGQQSLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
          MG  +LIY+ V+RGT +LA EYT F GNF+ IA QCL+KLPA+NNK TY  D HTFN+LV+
Sbjct   1      MGDANLIYSLVSRGTTVLA EYTSFAGNFSQIAMQCLVKLPAANNKHTYVMDRHTFNFLVQ 60

Query   61     DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DGFTY VVA E  G+QIP AF+DRVK+DF  RY GGKA  A ++SL+ EFG +LKEHM +
Sbjct   61     DGFTYLVVAEEDFGRQIPFAFLDRVKDDFKHRYQGGKADLAVSHSLDAEFGPRLKEHMDF 120

Query   121    CVDHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
          C  +PEE+ K++K+K+QV+EVKG+MMENI+KVL R EKI+LLVD+T +L+S A +F++QG
Sbjct   121    CERNPEEIRKMSKIKSQVAEVKGIMMENIDKVLVRNEKIDLLVDRTSHLQSDAHNFQRQG 180

Query   181    TNVRRKMWLQNMKIKLIVLGIILALILIIILSVCHGFKCH 220
          +R K+W QN ++KL+VL +II +  II LS+C GF C+
Sbjct   181    KKIRYKLWCQNYRLKLLVLVLIIIVAFIIYLSICRGFVCY 220

```

>ref|NP\_193313.2| **UG** ATVAMP724 (Arabidopsis thaliana vesicle-associated membran  
724)  
Length=194

GENE ID: 827258 ATVAMP724 | ATVAMP724 (Arabidopsis thaliana vesicle-associated  
membrane protein 724) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 275 bits (702), Expect = 2e-72, Method: Compositional matrix adjust.  
Identities = 128/189 (67%), Positives = 158/189 (83%), Gaps = 2/189 (1%)

```

Query   1      MGQQSLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNN-KFTYNCDGHTFNYLV 59
          MGQ+S IY+FVARGT+ILA EYTEFTGNF +IA+QCL KLP+S+N KFTYNCD HTFN+LV
Sbjct   1      MGQESFIYSFVARGTMILA EYTEFTGNFPSIAAQCLQKLPSSSNSKFTYNCDHHTFNFLV 60

Query   60     EDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQ 119
          ED + YCVVA +S+ +QI IAF++RVK DF KRYGGGKA+TA A SLN+EFG +KEHM
Sbjct   61     EDAYAYCVVAKDSLQISIAFLERVKADFKKRYGGGKASTAIKSLNKEFGPVMKEHMMN 120

Query   120    YCVDHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQ- 178
          Y VDH EE+ KL KVKAQVSEVK +M+ENI+K +DRGE + +L DKTENLRSQA+++++
Sbjct   121    YIVDHAEIEKLIKVKVKAQVSEVKSIMLENIDKAIDRGENLTVLTDKTENLRSQA REYKKT 180

Query   179    QGTNVRRKM 187
          +G RRK
Sbjct   181    KGHRWRRKF 189

```

>ref|XP\_001692216.1| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt  
gb|EDP04166.1| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]  
Length=219

GENE ID: 5717909 VAMP72 | R-SNARE protein, VAMP72-family  
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

Score = 268 bits (685), Expect = 2e-70, Method: Compositional matrix adjust.  
Identities = 126/210 (60%), Positives = 167/210 (79%), Gaps = 1/210 (0%)

```

Query   5      SLIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          LIYAFVARGT +LA EYT ++GNF T+A +CL KL          KFT  CD HTFN+LV +GFT
Sbjct   2      PLIYAFVARGTTVLA EYTPYSGNFNTVAIECLQKLANPEPKFTIACDRHTFNFLVANGFT 61

Query   65     YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          Y VVA E+ G+QIP AF++RV+++F ++Y  KA TAAA S++R FG +LK HM+YC+DH
Sbjct   62     YLVVADEAYGRQIPFAFLERV RDEFEEKYAE-KARTAAALSMDRTFGPRLKSHMEYCMDH 120

Query   125    PEEVSKLAKVKAQVSEVKGVMMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTNVR 184
          PEE+SK+A V+ +V+EVK VM+ENIEKVL+RGEKIELLV DKT++LR+QA+ F+++G +R
Sbjct   121    PEEISKIAAVQKKVNEVKDVMVENIEKVLERGEKIELLV DKTDDLNRNQA EQFKKGRQLR 180

```

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVC 214  
 KMW QN ++KLIVL I+ L ++I L VC  
 Sbjct 181 NKMWWQNCRMKLIVLFAILLAVVIFLLVC 210

>ref|NP\_001059291.1| **UG** Os07g0249200 [Oryza sativa (japonica cultivar-group)]  
 dbj|BAC20811.1| **G** putative Vesicle-associated membrane protein [Oryza sativa Ja Group]  
 dbj|BAD30660.1| **G** putative Vesicle-associated membrane protein [Oryza sativa Ja Group]  
 dbj|BAF21205.1| **G** Os07g0249200 [Oryza sativa (japonica cultivar-group)]  
 Length=248

GENE ID: 4342836 Os07g0249200 | Os07g0249200 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 266 bits (679), Expect = 9e-70, Method: Compositional matrix adjust.  
 Identities = 135/223 (60%), Positives = 175/223 (78%), Gaps = 9/223 (4%)

Query 6 LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNN-----KFTYNCDGHTFN 56  
 LIYAFVARGT +LAEYTEFTGNF +A+QCL +LPAS +F+Y CDGHTFN  
 Sbjct 23 LIYAFVARGTAVLAEYTEFTGNFPALAAQCLQRLPASGGGGSGGGAPARFSYACDGHTFN 82

Query 57 YLVEDGFTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE 116  
 +L+ G+ YCVVA ESV + + +AF++R+K+DF KRYGGGKA TA A SLN+E+G +K+  
 Sbjct 83 FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ 142

Query 117 HMQYCVDPHPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIELLVDKTENLRSQAQDF 176  
 HMQY +DH EE+ K KV+AQVSEVK +M+ENIEK L RGEK+ L DKT +L+SQAQ+F  
 Sbjct 143 HMQYVLDHSEEIEKTLKVQAQVSEVKNMLENIEKTLGRGEKLSLQDKTSDLQSQAQEF 202

Query 177 RQQGTNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219  
 +++G +RRK WLQNMKIKL+VLGI++ L++I+ +SVC GF C  
 Sbjct 203 KKGKVKIRKRTWLQNMKIKLVVLGILLLLVIIVWVSVCQGFDC 245

>gb|EAZ07996.1| hypothetical protein OsI\_029228 [Oryza sativa (indica cultivar-g  
 Length=633

Score = 263 bits (673), Expect = 5e-69, Method: Compositional matrix adjust.  
 Identities = 121/216 (56%), Positives = 162/216 (75%), Gaps = 20/216 (9%)

Query 2 QQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNLYLVED 61  
 +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP + +K TY+CDGHTFN+LV+  
 Sbjct 4 NKQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPNTSKSTYSCDGHTFNFLVDR 63

Query 62 GFTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGG-----KAATA 101  
 GF + VVA E+VG+ +P F+DRVKEDE +RYG + +  
 Sbjct 64 GFVFLVVADEAVGRSVPFVFLDRVKEDEFMQRYGSSIDEEGQHPLADDADDDDFLLEDRFS 123

Query 102 AANSLNREFGSKLKEHMQYCVDPHPEEVSKLAKVKAQVSEVKGVMENIEKVLDGRGEKIEL 161  
 A +L+REFG +LK+HM YC++HPEE+SKL+KVKA ++EVKG+MM+NIEK+L+RGEKIEL  
 Sbjct 124 IAYNLDREFGPRKLDHMLYCINHPPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIEL 183

Query 162 LVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLI 197  
 LV KTE L+SQA F + G +RRKMWLQN++ KL+  
 Sbjct 184 LVGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLM 219

>gb|EAZ43645.1| hypothetical protein OsJ\_027128 [Oryza sativa (japonica cultivar  
 Length=1259

Score = 263 bits (672), Expect = 7e-69, Method: Compositional matrix adjust.  
 Identities = 121/215 (56%), Positives = 162/215 (75%), Gaps = 20/215 (9%)

Query 3 QQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNLYLVEDG 62  
 +QSLIY+FVA+G+V+LAE+T F+GNF+TIA QCL KLP + +K TY+CDGHTFN+LV+ G  
 Sbjct 5 KQSLIYSFVAKGSVVLAEHTAFSGNFSTIAVQCLQKLPNTSKSTYSCDGHTFNFLVDRG 64

Query 63 FTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGG-----KAATAA 102  
 F + VVA E+VG+ +P F+DRVKEDE +RYG + +  
 Sbjct 65 FVFLVVADEAVGRSVPFVFLDRVKEDEFMQRYGSSIDEEGQHPLADDADDDDFLLEDRFSI 124

```

Query 103  ANSLNREFGSKLKEHMQYCVDPHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELL 162
           A +L+REFG +LK+HM YC++HPEE+SKL+KVKA ++EVKG+MM+NIEK+L+RGEKIELL
Sbjct 125  AYNLDREFGPRKLDHMLYCINHPPEEISKLSKVKAHLTEVKGIMMDNIEKILERGEKIELL 184

Query 163  VDKTENLRSAQDFRQQGTNVRKMWLQNMKIKLI 197
           V KTE L+SQA F + G +RRKMWLQN++ KL+
Sbjct 185  VGKTETLQSQADSFHRHGRELRRKMWLQNLRFKLM 219

```

>gb|AAC04922.1| putative synaptobrevin [Arabidopsis thaliana]  
Length=212

Score = 261 bits (668), Expect = 2e-68, Method: Compositional matrix adjust.  
Identities = 121/163 (74%), Positives = 142/163 (87%), Gaps = 0/163 (0%)

```

Query 1      MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
           M QQSL Y+F+ARGTVIL E+T+F GNFT++A+Q L LP+SNNKFTYNCDGHTFN LVE
Sbjct 1      MAQQSLFYFSFIARGTVILVEFTDFKGNFTSVAAQYLENLPSSNNKFTYNCDGHTFNDLVE 60

Query 61     DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
           +GFTYCVVAV+S G++IP+AF++RVKEDF KRYGG KAAT ANSLN+EFGS LKEHMQY
Sbjct 61     NGFTYCVVAVDSAGREIPMAFLERVKEDFYKRYGGEKAATDQANSLNKEFGSNLKEHMQY 120

Query 121    CVDHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLV 163
           C+DHP+E+S LAK KAQVSEVK +MMENIEKVL RG E+LV
Sbjct 121    CMDHPDEISNLAKAKAQVSEVKSMMENIEKVLARGVICEMLV 163

```

>gb|AAB80624.1| Strong similarity to Arabidopsis ATHSAR1 (gb|M90418). ESTs gb|T4  
come from this gene. [Arabidopsis  
thaliana]  
Length=175

Score = 260 bits (665), Expect = 4e-68, Method: Compositional matrix adjust.  
Identities = 137/157 (87%), Positives = 150/157 (95%), Gaps = 0/157 (0%)

```

Query 63      FTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
           F+YCVVAV+S G+QIP++F++RVKEDF KRYGGGKAATA ANSLN+EFGSKLKEHMQY+
Sbjct 19      FSYCVVAVDSAGRQIPMSFLERVKEDFNKRYGGGKAATAQANSLNKEFGSKLKEHMQYCM 78

Query 123     DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQGTN 182
           DHP+E+S LAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFR GT
Sbjct 79      DHPDEISKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRTTGTQ 138

Query 183     VRRKMWLQNMKIKLIVLGIILIALILIIILSVCHGFKC 219
           +RRKMWLQNMKIKLIVL IIALILII+LSVCHGFKC
Sbjct 139     MRRKMWLQNMKIKLIVLAIILIALILIIIVLSVCHGFKC 175

```

>ref|XP\_001764415.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
gb|EDQ70682.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
Length=238

Score = 260 bits (665), Expect = 5e-68, Method: Compositional matrix adjust.  
Identities = 120/220 (54%), Positives = 173/220 (78%), Gaps = 0/220 (0%)

```

Query 1      MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVE 60
           MG LIY+FVARGT +LAE+ + GNFT+ IA QCL+KLPA +K TY D HTFN+ VE
Sbjct 1      MGDARLIYSFVARGTTVLAEHAIYAGNFSQIAVQCLLKLPAAGTSKQTYVMDRHTFNFVE 60

Query 61     DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
           +GFT+ VVA E++G+ IP AF++RVK+DF Y GG+A A ++SL+ EFG KLKEHM +
Sbjct 61     NGFTFLVVAEEALGRLIPFAFLERVKDDFKHHYQGGRADLAVSHSLDAEFGPKLKEHMDF 120

Query 121    CVDHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSAQDFRQQG 180
           C+++PEE+ K++++K+QV+EVKG+MMENI+KVLDR +KI+LLVD+T +L+S A ++++ G
Sbjct 121    CMENPEEIKKISRIKSQVAEVKGIMMENIDKVLDRSDKIDLLVDRTHLQSSAAEYQRAG 180

Query 181    TNVRRKMWLQNMKIKLIVLGIILIALILIIILSVCHGFKCH 220
           +RR++W Q+ ++KL+VL +I+ + II LS+C GF CH
Sbjct 181    VRIRRLWWQHFRLLKLLVLLLVVAFIYLSICRGFICH 220

```

>gb|EAZ39281.1| hypothetical protein OsJ\_022764 [Oryza sativa (japonica cultivar Length=273

Score = 253 bits (646), Expect = 6e-66, Method: Compositional matrix adjust.  
Identities = 136/248 (54%), Positives = 176/248 (70%), Gaps = 34/248 (13%)

```

Query  6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNN-----KFTYNCDGHTFN  56
          LIYAFVARGT +LAEYTEFTGNF  +A+QCL +LPAS          +F+Y CDGHTFN
Sbjct  23  LIYAFVARGTAVLAEYTEFTGNFPALAAQCLQRLPASGGGGSGGGAPARFSYACDGHTFN  82

Query  57  YLVEDGFTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE  116
          +L+  G+  YCVVA  ESV  +  +  AF++R+K+DF  KRYGGGKA  TA  A  SLN+E+G  +K+
Sbjct  83  FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ  142

Query  117  HMQYCVDPHPEEVSKLAKVKAQVSEVKGVMMENIEKV-----  152
          HMQY +DH EE+ K  KV+AQVSEVK +M+ENIEKV
Sbjct  143  HMQYVLDHSEEIEKTLKVQAQVSEVKNMIMLENIEKVWSTFAVGCPLFFTELILMGFLFKK  202

Query  153  -LDRGEKIELLVDKTENLRSQAQDFRQOGTNVRRKMWLQNMKIKLIVLGIILIIIL  211
          L  RGEK+  L  DKT  +L+SQAQ+F+++G  +RRK WLQNMKIKL+VLGI++ L++I+  +
Sbjct  203  TLGRGEKLSELQDKTSDLSQAQEFKKKGVKIRRKTLWLQNMKIKLVVLGILLLLVVIWV  262

Query  212  SVCHGFKC  219
          SVC GF C
Sbjct  263  SVCQGFDC  270

```

>gb|EAZ25708.1| hypothetical protein OsJ\_009191 [Oryza sativa (japonica cultivar Length=183

Score = 252 bits (644), Expect = 1e-65, Method: Compositional matrix adjust.  
Identities = 123/217 (56%), Positives = 149/217 (68%), Gaps = 40/217 (18%)

```



Query  3  QQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNVLVEDG  62
          + +L+Y+FVARG V+L
Sbjct  6  RTTLVYSFVARGAVVLGRPRR-----  26

Query  63  FTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV  122
          YCVVA  ES  G+Q+P+  F++RVKEDF+K+Y  GGKA  A  ANSL  RE+G  KLKEHM+YC
Sbjct  27  -AYCVVATESAGRQLPVGFIERVKEDFSKKYSGGKAKNATANSKREYGPKLKEHMKYCD  85

Query  123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTN  182
          HP EE+  KLAKVKAQV+EVKGVM+NIKVLDRGEKIELLVDKTE+LRSQAQDFR+  GT
Sbjct  86  AHPEEIDKLAKVKAQVTEVKGVMQNIKVLDRGEKIELLVDKTEDLRSQAQDFRKAGTK  145

Query  183  VRRKMWLQNMKIKLIVLGIILIIILSVCHGFKC  219
          +RRKMW +NMK+KLIV  GI++ALIL+IIL+VC  C
Sbjct  146  IRRKMWWENMKMKLIVFGIVVALILVIILTVCRDLNC  182

```

>ref|XP\_001418265.1|  predicted protein [Ostreococcus lucimarinus CCE9901]  
gb|AB096558.1|  predicted protein [Ostreococcus lucimarinus CCE9901]  
Length=215

GENE ID: 5002283 OSTLU\_32248 | predicted protein  
[Ostreococcus lucimarinus CCE9901] (10 or fewer PubMed links)

Score = 246 bits (629), Expect = 6e-64, Method: Compositional matrix adjust.  
Identities = 118/214 (55%), Positives = 160/214 (74%), Gaps = 2/214 (0%)

```

Query  6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNVLVEDGFTY  65
          LIYAFVAR T +LAE+T ++GNF+TIA Q L KL  N +FTY  DGHTFN+VE+GFTY
Sbjct  3  LIYAFVARRTTVLAFTNYSGNFSTIAIQALEKLSDDNTRFTYTADGHTFN+VVENGFTY  62

Query  66  CVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDPH  125
          VVA  +G+  +P A  +DR+K  +FT+  +  +A  A  A+SLN+  F  +LKEH+++C  +P
Sbjct  63  LVVADSELGRHVPFACLDRIKSEFTRDHAS-EAQDAIAHSLNKSFAFRLKEHLEFCSANP  121

Query  126  EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTNVRR  185
          E  VSK++  V+  QVS+VK  +MM+NIKVLDRGEKIELLVDK++  LR  +A  +F  +  G  +RR
Sbjct  122  EAVSKVSAVQQQVSQVKEIMMDNIEKVLDRGEKIELLVDKSDALRFEAANFHKTGRALRR  181

Query  186  KMWLQNMKIKLIVLGIILIIILSVCHGFKC  219
          +W  QNMKIK+  II  AL+L  +I  ++C  G  KC

```

Sbjct 182 NLWCQNMKIKVAFGLIIFALLLTIFTLC-GKKC 214

>ref|XP\_001777794.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. pate  
gb|EDQ57456.1| **G** R-SNARE, VAMP72-family [Physcomitrella patens subsp. patens]  
Length=235

Score = 244 bits (622), Expect = 4e-63, Method: Compositional matrix adjust.  
Identities = 121/218 (55%), Positives = 157/218 (72%), Gaps = 0/218 (0%)

```
Query 3  QQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNKFTYNCDGHTFNYLVEDG 62
          ++ LIY+ FV+RGT +LAEY +GN IA+QCL KLP NNK TY CD HTFN+LVEDG
Sbjct 2  EEGLIYSFVSRGTTVLAEYASVSGNSNRIAAQCLAKLPGGNNKHTYVCDRHTFNFLVEDG 61

Query 63  FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
          FT+ VA E +QI AF+DRVK DF RY GG+A A SLN EFG +LKEHM +
Sbjct 62  FTFLAVADEDFSRQIAFAFLDRVKNDFQHRYQGGRADLAVTYSLNAEFGPRLKEHMDFA 121

Query 123  DHPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTN 182
          +PEE+ K++K+K+QV+EVK +MM NIEK+LDR E+I+LLV KT++L S A F +QG
Sbjct 122  ANPEEIKKMSKISQVAEVKEIMMVNIEKLLDRNERIDLLVGKTDLDHSAHVFEKQGNQ 181

Query 183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH 220
          +RR+ W + K+KL+VL +II + II LS+C F CH
Sbjct 182  IRRRAWCAHFKLKLLVLVLIIVAFIILYLSICRDFICH 219
```

>ref|NP\_001067392.1| **UG** Os12g0639800 [Oryza sativa (japonica cultivar-group)]  
gb|ABA99617.1| **G** Synaptobrevin family protein, expressed [Oryza sativa (japonic  
cultivar-group)]  
dbj|BAF30411.1| **G** Os12g0639800 [Oryza sativa (japonica cultivar-group)]  
Length=179

GENE ID: 4352920 Os12g0639800 | Os12g0639800 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 236 bits (602), Expect = 9e-61, Method: Compositional matrix adjust.  
Identities = 133/219 (60%), Positives = 152/219 (69%), Gaps = 40/219 (18%)

```
Query 1  MGQQSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNKFTYNCDGHTFNYLVE 60
          M + LIYA VARGTV+LAE+T + GNF IA+QCL KLPA +N+ TY CD HTFN+L+
Sbjct 1  MAESKLIYAMVARGTVVLAEHTAYAGNFRDIAAQCLQKLPAGDNRLTYTCDHTFNFLIH 60

Query 61  DGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          G+ YCVVA ES G+QIP+A +D +KEDF KR +L E M+Y
Sbjct 61  QGYAYCVVATESSGRQIPLALLDMIKEDFNKR-----PRLGEQMKY 101

Query 121  CVDHPEEVSKLAKVKAQVSEVKGVMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOG 180
          C+DHPEEVSKLAKVKAQVSEVKG+MMENI+K A DFRQOG
Sbjct 102  CMDHPEEVSKLAKVKAQVSEVKGIMMENIDK-----AADFRQOG 140

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKC 219
          T VRRKMW QNMKIKLIVLGIIIALILIIILSVCHGFKC
Sbjct 141  TRVRRKMWYQNMKIKLIVLGIIIALILIIILSVCHGFKC 179
```

>ref|XP\_001692208.1| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt  
gb|EDP04158.1| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]  
Length=218

GENE ID: 5717896 VAMP71 | R-SNARE protein, VAMP72-family  
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

Score = 217 bits (552), Expect = 6e-55, Method: Compositional matrix adjust.  
Identities = 107/209 (51%), Positives = 143/209 (68%), Gaps = 1/209 (0%)

```
Query 6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNKFTYNCDGHTFNYLVEDGFTY 65
          LIY+ V++GTV LAEY F+GNF +A L K + KFT+N DGHTFN+L GFTY
Sbjct 3  LIYSSVSQGTVTLAEYAAFSGNFGAVAKDYLEKAGKNEGKFTFNVDGHTFNFLNRGGFTY 62

Query 66  CVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP 125
```

```

Sbjct 63      VVA E+ G+ IP AF+D++ +F ++ KAA A LN FG +LK M++ +P
          LVVADEAYGRAIPSAFLDKMASEFAMKFAD-KAAGAKEGGLNGSFQKQLKSMMEHATQYP 121
Query 126     EEVSKLAKVKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR 185
          EE SK+A V+ +V EVKG+M ENIEKVL RGEK+ELL DKTENL ++A F++ G +RR
Sbjct 122     EEYSKVASVQKKVDEVKGIMTENIEKVLARGEKLELLTDKTENLMNEADRFQRTGRTLRR 181
Query 186     KMWLQNMKIKLIVLGIILIALILIIILSVC 214
          KMW QN K+K++V +I L ++I L VC
Sbjct 182     KMWWQNCKMKIVVALAVILLAVVIFLLVC 210

```

>gb|EAZ03380.1| hypothetical protein OsI\_024612 [Oryza sativa (indica cultivar-g  
Length=322

Sort alignments for this  
E value Score Percen  
Query start position

Score = 201 bits (511), Expect = 3e-50, Method: Compositional matrix adjust.  
Identities = 96/156 (61%), Positives = 121/156 (77%), Gaps = 9/156 (5%)

```

Query 6      LIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNN-----KFTYNCDGHTFN 56
          LIYAFVARGT +LA EYTEFTGNF +A+QCL +LPAS +F+Y CDGHTFN
Sbjct 23      LIYAFVARGTAVLA EYTEFTGNFPALAAQCLQRLPASGGGGSGGGAPARFSYACDGHTFN 82
Query 57      YLVEDGFTYCVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKE 116
          +L+ G+ YCVVA ESV + + +AF++R+K+DF KRYGGGKA TA A SLN+E+G +K+
Sbjct 83      FLLHRGYAYCVVAKESVPKNVSVAFLERLKDDFMKRYGGGKADTALAKSLNKEYGPVIKQ 142
Query 117     HMQYCVDPHPEEVSKLAKVKVKAQVSEVKGVMMENIEKV 152
          HMQY +DH EE+ K KV+AQVSEVK +M+ENIEKV
Sbjct 143     HMQYVLDHSEEIEKTLKVQAQVSEVKNIMLENIEKV 178

```

Score = 70.9 bits (172), Expect = 5e-11, Method: Compositional matrix adjust.  
Identities = 40/69 (57%), Positives = 56/69 (81%), Gaps = 0/69 (0%)

```

Query 151     KVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRRKMWLQNMKIKLIVLGIILIALILIII 210
          + L RGEK+ L DKT +L+SQAQ+F+++G +RRK WLQNMKIKL+VLGI++ L++I+
Sbjct 251     QTLGRGEKLSELQDKTSDLQSQAEFKKKGVKIRRKTLWLQNMKIKLVVLGILLLLVIVW 310
Query 211     LSVCHGFKC 219
          +SVC GF C
Sbjct 311     VSVCQGFDC 319

```

>ref|XP\_001692312.1| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt  
gb|EDP04262.1| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]  
Length=219

GENE ID: 5717794 VAMP74 | R-SNARE protein, VAMP72-family  
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

Score = 186 bits (472), Expect = 9e-46, Method: Compositional matrix adjust.  
Identities = 93/209 (44%), Positives = 129/209 (61%), Gaps = 0/209 (0%)

```

Query 6      LIYAFVARGTVILA EYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY 65
          L+Y V +G+V LA EY F GNF +A L K K Y DGH+ N+L GFTY
Sbjct 3      LVYVSVCQGSVALAEYAGFQGNFAVVARDYLDKATKLEGKSRYEVDGHSLNFLNRGGFTY 62
Query 66     CVVAVESVGQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDPH 125
          V+A G +P AF+D+V+ +F +YG G AAA SLN FG +LK+ + HP
Sbjct 63     LVIASVDSGVALPSAFLDKVEAEFRKYGAGLQLGAAAGSLNATFGKQLKQLTENATQHP 122
Query 126     EEVSKLAKVKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR 185
          EE SK+A V+ +V E K VM++NI+ VL RGEK+E + +KTE+L ++A FR V+R
Sbjct 123     EEFSKVA AVQKKVDEAKAVMVDNIDAVLKRGEKLEIQEKTEDLMAEADRFRDGAVRVKR 182
Query 186     KMWLQNMKIKLIVLGIILIALILIIILSVC 214
          K+W QN K+K++V +I L ++I L VC
Sbjct 183     KLWWQNCKMKIVVALAVILLAVVIFLLVC 211

```



>emb|CAL53602.1| SYNAPTOBREVIN-RELATED PROTEIN 1 (IC) [Ostreococcus tauri]  
Length=185

Score = 182 bits (462), Expect = 1e-44, Method: Compositional matrix adjust.  
Identities = 94/184 (51%), Positives = 138/184 (75%), Gaps = 2/184 (1%)

```
Query 36  LMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGG 95
          L K+   N +FTY DGHTFNY+VE+GFTY VVA S G+ +P A +DR+K +F + +
Sbjct 2   LEKISEDNTRFTYTADGHTFNYVVENGFTYLVVADSSQGRHVPFACLDRIKAEFARDHAS 61

Query 96  GKAATAAANSLNREFGSKLKEHMQYCVDPHEEVSKLAKVKAQVSEVKGVMMENIEKVLDR 155
          +A A A+SLN+ F +LKEH+++C +PE VSK+++V+ QVS+VK +MM+NIEKVLDR
Sbjct 62  -EAQDAIAHSLNKSFAFRLKEHLEFCSANPEAVSKVSQVQQQVSQVKEIMMDNIEKVLDR 120

Query 156  GEKIELLVDKTENLRSQAQDFRQOGTNNRRKMWLQNMKIKLIVLGIIIALILIIILSVCH 215
          GEKIE+LVDK++ LR QA +F + G +RR+MW +NMK+K++V I++A++ +I ++C
Sbjct 121  GEKIEILVDKSDALRFQADNFHKTGRQLRRRMWCENMKMKVLVGVIVLAILFTLIFTLC- 179

Query 216  GFKC 219
          G KC
Sbjct 180  GKKC 183
```

>ref|XP\_001692324.1| **UG** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardt  
gb|EDP04274.1| **G** R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]  
Length=220

GENE ID: 5717908 VAMP73 | R-SNARE protein, VAMP72-family  
[Chlamydomonas reinhardtii] (Over 10 PubMed links)

Score = 182 bits (462), Expect = 1e-44, Method: Compositional matrix adjust.  
Identities = 91/200 (45%), Positives = 125/200 (62%), Gaps = 2/200 (1%)

```
Query 16  VILAEYTEFTGNFTTIIASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTYCVVAVESVGQ 75
          V LAEY F GNF +A + L + K +Y DGHTF L GF + V A E+ G+
Sbjct 14  VTLAEYAAFAGNFGAVAKEYLAR-TTGEGLKSYAVDGHFTFTVLCRGGFVFLVAADDEATGK 72

Query 76  QIPIAFMDRVKEDFTKRYGGGKAATAAA-NSLNREFGSKLKEHMQYCVDPHEEVSKLAKV 134
          IP AF+D+V ++FT +Y A A L FG +LK M++ +PEE SK+A V
Sbjct 73  TIPSADFVDKVADEFTSKYADKAAGLAGKEGGLQSSFGKQLKSTMEHATQYPEEYSKVASV 132

Query 135  KAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTNNRRKMWLQNMKI 194
          + +V EVKG+M ENI+KVL RGEK+ELL DKTENL ++ F + G +RR+MW+QN K+
Sbjct 133  QKKVDEVKGIMTENIDKVLARGEKLELLTDKTENLMFESDRFVRTGRALRRRMWMQNCKM 192

Query 195  KLIVLGIIIALILIIILSVC 214
          K++V +I L ++I L VC
Sbjct 193  KIVVALAVILLAVVIFLLVC 212
```

>ref|NP\_196676.1| **UG** ATVAMP713 (Arabidopsis thaliana vesicle-associated membran  
713)

sp|Q9LFP1|VA713 ARATH **G** Vesicle-associated membrane protein 713 (AtVAMP713)

emb|CAB96650.1| **G** putative protein [Arabidopsis thaliana]

gb|AAM14024.1| **G** unknown protein [Arabidopsis thaliana]

gb|AAM67467.1| **G** unknown protein [Arabidopsis thaliana]  
Length=221

GENE ID: 830984 ATVAMP713 | ATVAMP713 (Arabidopsis thaliana vesicle-associated  
membrane protein 713) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 167 bits (424), Expect = 4e-40, Method: Compositional matrix adjust.  
Identities = 86/215 (40%), Positives = 141/215 (65%), Gaps = 6/215 (2%)

```
Query 5  SLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG 62
          ++I+A VARGTV+L+E++ + N ++I+ Q L KLP S++ +Y+ D + F+ DG
Sbjct 2  AIIFALVARGTVVLSEFSATSNASSISKQILEKLPGNDSDSHMSYSQDRYIFHVKRTDG 61

Query 63  FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
          T +A E+ G+ IP AF+D + + F K YG +A A S+N EF L + M++
Sbjct 62  LTVLCMADETAGRNIFFAFLDDIHQRFVKTYGRA-IHSAQAYSMMNDEFSSRVLSQQMEFYS 120
```

```

Query 123  DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN 182
+ P      +++++K ++S+V+ VM+ENI+KVLDRGE++ELLVDKTEN++ FR+Q
Sbjct 121  NDPN-ADMSRIKGEMSQVRNVMIEIDKVLDRGERLELLVDKTENMQGNTFRFRKQARR 179

Query 183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
R MW +N+K+ I L +++AL++ I ++ VCHG
Sbjct 180  YRTIMWWRNVKLT-IALILVLALVVYIAMAFVCHG 213

```

>ref|NP\_197628.1| **UG** ATVAMP714 (Vesicle-associated membrane protein 714) [Arabidopsis thaliana]

sp|Q9FMR5|VA714\_ARATH **G** Vesicle-associated membrane protein 714 (AtVAMP714)

dbj|BAB08335.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]  
Length=221

GENE ID: 832297 ATVAMP714 | ATVAMP714 (Vesicle-associated membrane protein 714) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 161 bits (408), Expect = 2e-38, Method: Compositional matrix adjust.  
Identities = 79/214 (36%), Positives = 137/214 (64%), Gaps = 4/214 (1%)

```

Query 5      SLIYAFVARGTVILAETFTGNFTTASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG 62
+++YA VARGTV+LAE++ TGN + + L KL S+ + ++ D + F+ L DG
Sbjct 2      AIVYAVVARGTVVLAEFSAVTGNTGAVVRRILEKLSPEISDERLCFSQDRYIFHILRSDG 61

Query 63     FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
T+ +A ++ G+++P +++ + F K YG A A A ++N EF L + M++
Sbjct 62     LTFLCMANDTFGRRVPFSSYLEEIHMRFMKNYK-VAHNAPAYAMNDEFSSRVLHQMEFFS 120

Query 123    DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN 182
+P V L +V+ +VSE++ VM+ENIEK+++RG++IELLVDKT ++ + FR+Q
Sbjct 121    SNPS-VDTLNRVRGEVSEIRSVMVENIEKIMERGDRIELLVDKTATMQDSSSFHFRKQSKR 179

Query 183    VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
+RR +W++N K+ +++ +I+ L+ III S C G
Sbjct 180    LRRALWMKNAKLLVLLTCLIVFLLYIIIASFCGG 213

```

>gb|ABM30199.2| synaptobrevin-like protein [Brassica juncea]  
Length=221

Score = 161 bits (408), Expect = 3e-38, Method: Compositional matrix adjust.  
Identities = 79/214 (36%), Positives = 138/214 (64%), Gaps = 4/214 (1%)

```

Query 5      SLIYAFVARGTVILAETFTGNFTTASQCLMKLPA--SNNKFTYNCDGHTFNYLVEDG 62
++IYA VARGTV+LAE++ TGN + + L KL ++ + ++ D + F+ L DG
Sbjct 2      AIIYAVVARGTVVLAEFSAVTGNTDAVVRRILEKLSPETADERLCFSQDRYIFHILRSDG 61

Query 63     FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
T+ +A ++ G++IP +++ ++ F K YG A A A ++N EF L + M++
Sbjct 62     LTFLCMANDTFGRRIPFSSYLEEIQMRFMKNYK-VAHQAPAYAMNDEFSSRVLHQMEFFS 120

Query 123    DHPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN 182
+P V L +V+ +VSE++ VM++NIEK+++RG++IELLVDKT ++ A FR+Q
Sbjct 121    SNPS-VDTLNRVRGEVSEIRSVMDNIEKIMERGDRIELLVDKTATMQDSAFHFRKQSKR 179

Query 183    VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
+RR +W++N K+ +++ +I+ ++ III S C G
Sbjct 180    LRRALWMKNAKLLVMLTCVIVLVLYIIIASFCGG 213

```

>pir|B71423 hypothetical protein - Arabidopsis thaliana  
emb|CAB10356.1| SYBL1 like protein [Arabidopsis thaliana]  
emb|CAB78620.1| SYBL1 like protein [Arabidopsis thaliana]  
Length=159

Score = 160 bits (405), Expect = 5e-38, Method: Compositional matrix adjust.  
Identities = 82/146 (56%), Positives = 98/146 (67%), Gaps = 35/146 (23%)

```

Query 1      MGQQSLLIYAFVARGTVILAETFTGNFTTASQCLMKLP-ASNNKFTYNCDGHTFNYLV 59
MGQ+S IY+FVARGT+ILAETFTGNF +IA+QCL KLP +SN+KFTYNCD HTFN+LV
Sbjct 1      MGQESFIYSFVARGTMILAETFTGNFPSIAAQCLQKLPSSSNSKFTYNCDHHTFNFLV 60

```

```

Query 60 EDG-----FTYCVVAVESVGQIQPIAFMDRV 85
          ED          + YCVVA +S+ +QI IAF++RV
Sbjct 61 EDAYGWSLSLSSSLETNNLYLLWFGDETHMCFKIICYAYCVVAKDSLKQISIAFLERV 120

Query 86 KEDFTKRYGGGKAATAAANSLNREFG 111
          K DF KRYGGGKA+TA A SLN+EFG
Sbjct 121 KADFKKRYGGGKASTAIAKSLNKEFG 146

```

>ref|NP\_194942.1| **UG** VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C) [Arabidops thaliana]

sp|O49377|VA711 ARATH **G** Vesicle-associated membrane protein 711 (AtVAMP711) (v-synaptobrevin 7C) (AtVAMP7C)

gb|AAL27509.1|AF439840\_1 **G** AT4g32150/F10N7\_40 [Arabidopsis thaliana]  
6 more sequence titles

emb|CAA16574.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

gb|AAD01748.1| **G** vesicle-associated membrane protein 7C; synaptobrevin 7C [Arab thaliana]

emb|CAB79933.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

gb|AAM65673.1| **G** synaptobrevin-like protein [Arabidopsis thaliana]

gb|AAM78063.1| **G** AT4g32150/F10N7\_40 [Arabidopsis thaliana]

dbj|BAE98551.1| **G** vesicle-associated membrane protein 7C [Arabidopsis thaliana]  
Length=219

GENE ID: 829347 VAMP7C | VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C)  
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.  
Identities = 80/213 (37%), Positives = 137/213 (64%), Gaps = 3/213 (1%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNK-FTYNC DGHTFNYLVEDGF 63
        +++YA VARGTV+L+E+T + N +TIA Q L K+P N+ +Y+ D + F+ DG
Sbjct 2 AILYALVARGTVVLSEFTATSTNASTIAKQILEKVP GDNDSNVSYSDRYVFHV KRTDGL 61

Query 64 TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
        T +A E+ G++IP AF++ + + F + YG TA A ++N EF L + + Y +
Sbjct 62 TVLCMAEETAGRRIPFAFLEDIHQRFVRTYGRA-VHTALAYAMNEEFSRVLSQQIDYYSN 120

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLV DKTENLRSQAQDFRQOGT NV 183
        P ++ ++K ++++V+GVM+ENI+KVLDRGE++ELLVDKT N++ FR+Q
Sbjct 121 DPN-ADRINRIKGEMNQVRGVMNIENIDKVLDRGERLELLVDKTANMQGNTFRFRKQARRF 179

Query 184 RRKMWLQNMKIKLIVLGI IIALILIIILSVCHG 216
        R +W +N K+ ++++ +++ +I I + +CHG
Sbjct 180 RSNVWWRNCKLTVLLILL LLLVIIYI AVAFLCHG 212

```

>emb|CA044255.1| unnamed protein product [Vitis vinifera]  
Length=220

Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.  
Identities = 73/214 (34%), Positives = 135/214 (63%), Gaps = 3/214 (1%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNK-FTYNC DGHTFNYLVEDGF 63
        +++YA VARG+++LAE++ + N + IA Q L K+P N+ +Y+ D + F+ DG
Sbjct 2 TILYALVARGSLVLAEFSGTSTNASAIARQILEKIPGDNDSNVSYSDRYIFHV KRTDGL 61

Query 64 TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
        T +A ++ G++IP AF++ + + F + YG +A A ++N +F L + M+Y +
Sbjct 62 TVLCMADDTAGRRIPFAFLEDIHQRFVRTYGRA-VHSAQAYAMNDDFSRVLSQQMEYYSN 120

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLV DKTENLRSQAQDFRQOGT NV 183
        P ++ ++K ++ +V+ VM+ENI+KVLDRG+++ELLVDKT N++ FR+Q
Sbjct 121 DPN-ADRINRLKGEMGQVRNVMNIENIDKVLDRGDRLELLVDKTANMQGNTFRFRKQARRF 179

Query 184 RRKMWLQNMKIKLIVLGI IIALILIIILSVCHGF 217
        R +W +N+K+ + ++ I++ ++ +I+ CHG

```

Sbjct 180 RSTVWWRNVKLTVALIIILLVIVYVILAFACHGL 213

>ref|XP\_001762112.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa  
gb|EDQ73216.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]  
Length=220

Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.  
Identities = 77/191 (40%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```
Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF 63
          +++YA VARGTV+LAE++ +GN +TIA + L KLP +++ +Y+ D H F+ L DG
Sbjct 2  AILYALVARGTVVLAEFSAASGNASTIARRILEKLPPGGDSRVSYSDRHIFHILKADGL 61

Query 64  TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
          T+ +A +S G++IP A+++ + F K YG A+TA A ++N EF L + M+Y
Sbjct 62  TFLCMATDSFGRRIPFAYLEDIHMRFMKNYK-VASTALAYTMNDEF SRVLHQQMEYFST 120

Query 124  HPEEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQOGTNV 183
          + ++ + +VK ++ EV+ VM+ENI+KVL+RG++IELLV DKT ++ F++Q +
Sbjct 121  N-KQADSINRVKGEIVEVRAVMVENIDKVLERG DRIELLV DKTATI QDNTFRFKQSRRL 179

Query 184  RRKMWLQNMKI 194
          R+ MW++N K+
Sbjct 180  RQAMWIKNAKL 190
```

>ref|NP\_001064184.1| **UG** Os10g0154000 [Oryza sativa (japonica cultivar-group)]  
gb|ABB46773.2| **G** Synaptobrevin family protein, expressed [Oryza sativa (japonic  
cultivar-group)]  
dbj|BAF26098.1| **G** Os10g0154000 [Oryza sativa (japonica cultivar-group)]  
Length=226

GENE ID: 4348130 Os10g0154000 | Os10g0154000 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 156 bits (394), Expect = 1e-36, Method: Compositional matrix adjust.  
Identities = 79/221 (35%), Positives = 134/221 (60%), Gaps = 9/221 (4%)

```
Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPA-SNNKFTYNCDGHTFNYL----- 58
          +++YA VARGTV+LAE++ +GN +A + L KLP + ++ + D + F+ L
Sbjct 2  AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP 61

Query 59  -VEDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH 117
          DG T+ +A ++ G++IP +++ ++ F K YG A A A ++N EF L +
Sbjct 62  AAADGLTFLCMANDTFGRRIPFLYLEDIQMRFIKKNYGR-IAHNALAYAMNDEF SRVLHQQ 120

Query 118  MQYCVDHPEEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFR 177
          M+Y +P L +++ +VSE+ VM++NIEK+LDRGE+I LLVDKT ++ A FR
Sbjct 121  MEYFSSNPS-ADTLNRLRGEVSEIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR 179

Query 178  QOGTNVRRKMWLQNMKIKLIVLGIILILIIILSVCHGFK 218
          +Q +RR +W++N K+ ++ +I+ L+ +II + C G
Sbjct 180  KQSRRLRRALWMKNAKL L AVLTA VIV LLLYLI IIAAFCGGLS 220
```

>ref|XP\_001778044.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa  
gb|EDQ57153.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]  
Length=220

Score = 155 bits (392), Expect = 2e-36, Method: Compositional matrix adjust.  
Identities = 75/191 (39%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```
Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF 63
          +++YA VARGTV+LAE++ +GN +TIA + L K+P +++ +Y+ D H F+ + DG
Sbjct 2  TILYALVARGTVLLAEFSAASGNSTIARRILEKIPPGDSRVSYSDRHIFHIMKADGL 61

Query 64  TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
          T+ +A +S G++IP +++++ + F K YG A+TA A ++N EF L + M+Y
Sbjct 62  TFLCMASDSFGRRIPFSYLEDIHMRFMKNYK-VASTALAYAMNDEF SRVLHQQMEYFSR 120
```

```

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV 183
          +P      + +VK +++EV+ VM+ENI+KVL+RG++IELLVDKT ++      F++Q +
Sbjct 121 NPN-ADTINRVKGEIAEVRAVMVENIDKVLERGDRIELLVDKTSTIQDNTFRFKKQSRRL 179

Query 184 RRKMWLQNMKI 194
          R+ MW++N K+
Sbjct 180 RQAMWMKNAKL 190

```

>ref|XP\_001631076.1| **G** predicted protein [Nematostella vectensis]

gb|ED039013.1| **G** predicted protein [Nematostella vectensis]  
Length=223

GENE ID: 5510622 NEMVEDRAFT\_vlg209672 | predicted protein  
[Nematostella vectensis] (10 or fewer PubMed links)

Score = 155 bits (391), Expect = 2e-36, Method: Compositional matrix adjust.  
Identities = 72/212 (33%), Positives = 125/212 (58%), Gaps = 1/212 (0%)

```

Query 6 LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY 65
          ++Y+ V+RGT +LA++ GNF + Q L ++P N+K TY + F+Y+ ED Y
Sbjct 3 ILYSVVSRGTTVLAKFAACAGNFAEVTEQILSRIPPDNSKLTYTQGSYLFHYISEDRIIY 62

Query 66 CVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDP 125
          + ++ + ++ +K F Y G +A TA ++N EF L M++ D
Sbjct 63 LCITDDAFERSQAFLYLTEIKRRFQAAYHG-RAQTALPFAMNSEFSRVLSAEMKHYSR 121

Query 126 EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR 185
          EE S +AKV+ ++ E++G+M++NI+ + RGE++ELL+DK E+L S + F++ + R
Sbjct 122 EEGSSIAKVQVELDEIRGIMVKNIDSIASRGERLELLIDKAEDLNSSSLTFKKTSGRLAR 181

Query 186 KMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
          MW +N+KI LI++ I I +I I+ + C+G
Sbjct 182 AMWWKNVKITLILIAISIVVIYFIVSAACNGL 213

```

>ref|XP\_001769494.1| **UG** R-SNARE, VAMP71-family [Physcomitrella patens subsp. pa

gb|EDQ65655.1| **G** R-SNARE, VAMP71-family [Physcomitrella patens subsp. patens]  
Length=220

Score = 154 bits (389), Expect = 5e-36, Method: Compositional matrix adjust.  
Identities = 73/191 (38%), Positives = 128/191 (67%), Gaps = 3/191 (1%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLP-ASNNKFTYNCDGHTFNYLVEDGF 63
          +++YA VARGTV+LAE++ +GN +TIA + L K+P +++ +Y+ D H F+ + DG
Sbjct 2 TILYALVARGTVVLAEFSAASGNSSTIARRILEKIPPGGDSRVSYSDRHIFHIMKADGL 61

Query 64 TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDP 123
          T+ +A ++ G++IP ++++ + F K YG +A+TA A ++N EF L + M+Y
Sbjct 62 TFLCMASDTFGRRIPFSYLEDIHMRFMKSYGK-VASTALAYAMNDEFSRVLHQQMEYFSS 120

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNV 183
          +P      + +VK +++EV+ VM+ENI+KVL+RG++IELLVDKT ++      F++Q +
Sbjct 121 NPN-ADTINRVKGEIAEVRAVMVENIDKVLERGDRIELLVDKTSTIQDNTFRFKKQSRQL 179

Query 184 RRKMWLQNMKI 194
          ++ MW++N K+
Sbjct 180 KQAMWMKNAKL 190

```

>gb|ABK93000.1| unknown [Populus trichocarpa]  
Length=220

Score = 150 bits (380), Expect = 4e-35, Method: Compositional matrix adjust.  
Identities = 77/214 (35%), Positives = 137/214 (64%), Gaps = 3/214 (1%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNK-FTYNCDGHTFNYLVEDGF 63
          +++YA VARG+V+LAE+T N + IA Q L K+P +++ +Y+ D + F+ DG
Sbjct 2 AILYALVARGSVVLAEFSTATNASAIARQILDKIPGNDNSVSYSDRYIFHVKRTDGL 61

Query 64 TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDP 123
          T +A E+ G++IP AF++ + + F + YG TA A ++N EF L + M+Y +
Sbjct 62 TVLCMADETAGRRIPFAFLEDIHQRFVRTYGRA-VITAQAYAMNDEFSRVLSSQMEYYTN 120

```

```

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGTNV 183
          P      ++ ++K ++S+V+ VM+ENI+KVL+RG+++ELLVDKT N++      FR+Q
Sbjct 121 DPN-ADRINRLKGEMSQVRNVMNIENIDKVLGERDRLELLVDKTANMQGNTFRFRKQARRF 179

Query 184 RRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
          R  +W +N+K+ + ++ +++ +I.+++ VCHG
Sbjct 180 RSTVWWRNVKLTVALILLLLVIIYVVLAFVCHGL 213

```

>ref|XP\_001698008.1| **UG** R-SNARE protein, VAMP71-family [Chlamydomonas reinhardt  
gb|EDO99593.1| **G** R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii]  
Length=218

GENE ID: 5723646 VAMP75 | R-SNARE protein, VAMP71-family  
[Chlamydomonas reinhardtii] (10 or fewer PubMed links)

Score = 150 bits (379), Expect = 6e-35, Method: Compositional matrix adjust.  
Identities = 85/214 (39%), Positives = 124/214 (57%), Gaps = 5/214 (2%)

```

Query 4  QSLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGF 63
          Q.++++ VARG V+LAE      TGN  IA + L KLP  + + +Y  +  F+ +V DG
Sbjct 5  QKILFSLVARGQVVLAE--NRVTGNVNVIAVRILEKLPHEDTRVSYTQERFMFHVMSDGI 63

Query 64  TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
          TY  VA E  G++IP AF+D V+  F  YG  A  A  A  N EF  L E  +  D
Sbjct 64  TYMAVAEEGFGRRIFFAFLDDVRGRFVAMYGVA-AKEAVAYEYNTFEFSRVLAERAAHFSD 122

Query 124 HPEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGTNV 183
          +  + +VK ++ EVK +M+ENIEKVL+RGE+++LLVDKTE L+  + FR++  +
Sbjct 123 PSADA--INRVKGELQEVKHIMIENIEKVLGERGERLDLLVDKTEGLQQVSLAFRREARRL 180

Query 184 RRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
          +  MW +N K+ ++V      LI  I+  VC GF
Sbjct 181 KHTMWWKNAKLWVLVCAATALLIYFILGMVC-GF 213

```

>ref|XP\_001745842.1| **G** predicted protein [Monosiga brevicollis MX1]  
gb|EDQ89266.1| **G** predicted protein [Monosiga brevicollis MX1]  
Length=236

Score = 149 bits (376), Expect = 1e-34, Method: Compositional matrix adjust.  
Identities = 77/195 (39%), Positives = 119/195 (61%), Gaps = 4/195 (2%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          +LIYA VAR  ILAE+TE +GNFTT+  L K+P S+ + TY  D + F+Y+ EDG
Sbjct 3  ALIYALVARDNTILAEFTENSGNFTTQTSILDKIPNSDQRTYVYDRYLFHYVREDGIV 62

Query 65  YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          Y  +A ES G++ P AF+ ++ +DF      K++ A A  LNREF  LK  M
Sbjct 63  YLCLADESFGRRAPFAFLAQIMKDFKPYKSASKSSIAYA--LNREFAPVLKRQMAAFNKG 120

Query 125 PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSAQDFRQQGTNVR 184
          ++  L + + ++  VK VM+ENIEKVL RGE+I+++V+K E+L  +++ F+  ++
Sbjct 121 SDDA--LDRARGEIEGVKHMVENIEKVLQRGEQIDIMVEKAEDLSHESKRFTSARKLK 178

Query 185 RKMWLQNMKIKLIVL 199
          +MW +N K  L++
Sbjct 179 NRMWWENQKFCLLLF 193

```

>ref|XP\_001879548.1| **G** VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H  
gb|EDR10163.1| **G** VAMP/synaptobrevin-like protein [Laccaria bicolor S238N-H82]  
Length=224

Score = 148 bits (373), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 79/211 (37%), Positives = 132/211 (62%), Gaps = 8/211 (3%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          SLI+A VA+GT +LAE+      +F+      L K+P +N+K TY  + + F+Y+ EDG+T
Sbjct 2  SLIHALVAKGTTVLAEHKAGGRDFSQATQTILSKIPPNNKLTAYAEQYQFHYISEDGYT 61

```

```

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATA--AANSLNREFGSKLKEHMQ-Y 120
          Y V+A +SVG++ AF+ ++ FT      +++      A SL FG + +Q Y
Sbjct 62 YLVMADDSVGRRTSFAFLADLQRFKTAAPSSSSSSSQDEIPAYSLQGSFGPTISALLQTY 121

Query 121 CVDHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQG 180
          P + +LA+ + ++++VK +M++N+E++L RGE+IELLVDKT+ + QA FR+
Sbjct 122 NTAPPSD--ELARAQNELNQVKDIMVQNVEQILSRGERIELLVDKTDVMAGQATAFRGA 179

Query 181 TNVRRKMWLQNMKIKLIVLGIILILILIIIL 211
          +VRR+MW +N K+I L +++AL L+ +L
Sbjct 180 RSVRRQMWWKNS--KMIALSVVVALFLLWLL 208

```

>gb|EAY77730.1| hypothetical protein OsI\_031689 [Oryza sativa (indica cultivar-g Length=223

Score = 146 bits (369), Expect = 9e-34, Method: Compositional matrix adjust.  
Identities = 77/221 (34%), Positives = 131/221 (59%), Gaps = 12/221 (5%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPA-SNNKFTYNCDGHTFNYL----- 58
          +++YA VARGTV+LAE++ +GN +A + L KLP + ++ + D + F+ L
Sbjct 2 AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP 61

Query 59 -VEDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH 117
          DG T+ +A ++ G++IP +++ ++ F K YG A A A ++N EF L +
Sbjct 62 TAADGLTFLCMANDTFGRRIPLYLEDIQMRFIKNYGR-IAHNALAYAMNDEF SRVLHQ 120

Query 118 MQYCVDPHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSQAQDFR 177
          M+Y +P L +++ E+ VM++NIEK+LDRGE+I LLVDKT ++ A FR
Sbjct 121 MEYFSSNPS-ADTLNRLRG---EIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR 176

Query 178 QQGTNVRRKMWLQNMKIKLIVLGIILILILIIILSVCHGFK 218
          +Q +RR +W++N K+ ++ +I+ L+ +II + C G
Sbjct 177 KQSRRLRRALWMKNALLAVLTAVIVLLLYLIIIAAFCGGLS 217

```

>gb|AAM14694.1|AC097446\_23 Putative synaptobrevin-like protein [Oryza sativa (ja  
gb|EAZ15333.1| hypothetical protein OsJ\_029542 [Oryza sativa (japonica cultivar Length=223

Score = 146 bits (369), Expect = 9e-34, Method: Compositional matrix adjust.  
Identities = 77/221 (34%), Positives = 131/221 (59%), Gaps = 12/221 (5%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPA-SNNKFTYNCDGHTFNYL----- 58
          +++YA VARGTV+LAE++ +GN +A + L KLP + ++ + D + F+ L
Sbjct 2 AIVYAVVARGTVVLAEFSAVSGNAGAVARRILEKLPPDAESRLCFAQDRYIFHVLRSPPP 61

Query 59 -VEDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEH 117
          DG T+ +A ++ G++IP +++ ++ F K YG A A A ++N EF L +
Sbjct 62 AAADGLTFLCMANDTFGRRIPLYLEDIQMRFIKNYGR-IAHNALAYAMNDEF SRVLHQ 120

Query 118 MQYCVDPHPPEEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSQAQDFR 177
          M+Y +P L +++ E+ VM++NIEK+LDRGE+I LLVDKT ++ A FR
Sbjct 121 MEYFSSNPS-ADTLNRLRG---EIHTVMVDNIEKILDRGERISLLVDKTSTMQDSAFHFR 176

Query 178 QQGTNVRRKMWLQNMKIKLIVLGIILILILIIILSVCHGFK 218
          +Q +RR +W++N K+ ++ +I+ L+ +II + C G
Sbjct 177 KQSRRLRRALWMKNALLAVLTAVIVLLLYLIIIAAFCGGLS 217

```

>ref|XP\_642704.1| **UG** synaptobrevin domain-containing protein [Dictyostelium dis AX4]  
sp|Q86AQ7.1|VAM7B DICDI Vesicle-associated membrane protein 7B  
gb|AA051196.1| similar to Arabidopsis thaliana (Mouse-ear cress). Synaptobrevin protein [Dictyostelium discoideum]  
gb|EAL68772.1| **G** synaptobrevin domain-containing protein [Dictyostelium discoid AX4]  
Length=260

GENE ID: 3393839 vamp7B | longin domain-containing protein  
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 146 bits (368), Expect = 1e-33, Method: Compositional matrix adjust.

Identities = 79/214 (36%), Positives = 132/214 (61%), Gaps = 3/214 (1%)

```

Query 6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVEDGFTY 65
        +IY+ VARG+ +LAE+T  GNF TI  + L  +P ++ K +Y  + + F+YLV D  TY
Sbjct 3  IIYSLVARGSSVLA EFTSTNGNFVTITRRILDLIPPNDTKMSYVYEKYIFHYLVSDTLTY 62

Query 66  CVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV DHP 125
        +A E  G++IP  F+D VK  F  Y G K  TA A  +N +F  L+  M +  +
Sbjct 63  LCMAD EEFGRRI PF TFLDDVKNRFKSMY-GDKGKTAIAYGMNSDFSRTLENLMDH-YSNT 120

Query 126  EEVSKLAKVKAQVSEVKGVM MENI-EKVLDRGEKIELLV DKTENLRSQAQDFRQOGTNVR 184
        V  +++  A++ EVK +++ +I  ++L RGEKIE+LV++T+ L  Q+  F++Q  ++
Sbjct 121  TRVD TMSRTMAEIDEVKNILVSDIAPQLLKRGEKIEMLVERTDTLNQQSFKFKKQSKQLK 180

Query 185  RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFK 218
        MW +N+K+ L++  I++ +I II++S C GF+
Sbjct 181  CAMWWKNV KLMVLVGAIVLIIIFIIVMSYCDGFR 214

```

>ref|NP\_001056946.1| **UG** Os06g0174400 [Oryza sativa (japonica cultivar-group)]  
 dbj|BAA95814.1| **G** putative synaptobrevin 1 [Oryza sativa Japonica Group]  
 dbj|BAF18860.1| **G** Os06g0174400 [Oryza sativa (japonica cultivar-group)]  
 Length=221

GENE ID: 4340278 Os06g0174400 | Os06g0174400 [Oryza sativa Japonica Group]  
 (10 or fewer PubMed links)

Score = 145 bits (367), Expect = 1e-33, Method: Compositional matrix adjust.  
 Identities = 72/215 (33%), Positives = 133/215 (61%), Gaps = 4/215 (1%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLP A--SNNKFTYNC DGHTFNYLVEDG 62
        +++YA VARGTV+LAE++  N  +A Q L +LP  +++  +Y  D + F+  DG
Sbjct 2  AILYAVVARGTVVLA EHSAAATNAGAVARQVLERLP GGGADSHVSYTQDRYVFHAKRTDG 61

Query 63  FTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV 122
        T  +A E+ G++IP AF++ +  F K YG  A T+ A  +N EF  L + M Y
Sbjct 62  ITALCMAD E AAGRRIPFAFLEDIHGRFVKTYGRA-ALTS LAYGMNDEF SRVLSQQMDYY S 120

Query 123  DHPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQOGTN 182
        + P  ++ +++ ++S+V+ VM++NI+KVL+RG+++++LVDKT N++  F++Q
Sbjct 121  NDPN-ADRINRMGEISQVRTVMIDNIDKVLERGDR L DMLVDKTANMQGNTIRFKRQARR 179

Query 183  VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
        R  W +N+K+ + ++ ++  +I ++++ +CHGF
Sbjct 180  FRNTTWRNVKLTIALIFLLTVIIYVVLVFMCHGF 214

```

>gb|ABK95432.1| unknown [Populus trichocarpa]  
 Length=220

Score = 145 bits (366), Expect = 2e-33, Method: Compositional matrix adjust.  
 Identities = 74/213 (34%), Positives = 135/213 (63%), Gaps = 3/213 (1%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNK-FTYNC DGHTFNYLVEDGF 63
        +++YA VARG+V+LAE++  N  + IA Q L K+P +++  +Y+ D + F+  DG
Sbjct 2  AILYALVARGSVVLA EFSSTATNASAIARQILDKIPGNDDSNVSYSQDRYIFHVKRTDGL 61

Query 64  TYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCV D 123
        +A E+ G++IP AF++ + + F + YG  TA A ++N EF  L + M+Y  +
Sbjct 62  AVLCMAD ETAGRRIPFAFLEDIHQRFARTYGRA-VITAQAYAMNDEF SRVLSQQMEYYTN 120

Query 124  HPEEVSKLAKVKAQVSEVKGVM MENIEKVLDRGEKIELLV DKTENLRSQAQDFRQOGTNV 183
        P  ++ ++K ++S+V+ VM+ENI+KVL+RG+++ELLVDKT N++  FR+Q
Sbjct 121  DPN-ADRINRLKGEMSQVRNVM IENIDKVLERGDRLELLVDKTANMQGNTFRFRKQARRF 179

Query 184  RRMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
        +W +N+K+ + ++ +++ +I +++  VCHG
Sbjct 180  SSAVWWRNVKLTVALILLLVIIYVVLAVVCHG 212

```

>ref|XP\_001635801.1| **G** predicted protein [Nematostella vectensis]  
 gb|ED043738.1| **G** predicted protein [Nematostella vectensis]



Length=218

GENE ID: 5515684 NEMVEDRAFT vlgl83227 | predicted protein  
[Nematostella vectensis] (10 or fewer PubMed links)

Score = 140 bits (354), Expect = 5e-32, Method: Compositional matrix adjust.  
Identities = 74/191 (38%), Positives = 111/191 (58%), Gaps = 3/191 (1%)

```
Query 6  LIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNNKFTYNC DGHTFNYLVEDGFTY 65
          L Y+ +ARG IL +Y E TGNF + L K+P ++ K TY + F+ +VEDG Y
Sbjct 3  LYYSLIARGGTILVDYAETTGNFQQVTTYTILEKIPGNDTKCTYVSGSYQFHVIVEDGLVY 62

Query 66  CVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP 125
          +A + G++ P AF++ +K F+ +A TA + R+F L M D P
Sbjct 63  LCMADKEFGKKDPYAFLEEIKRRFSNSSLKARARTAQSFEFKRDFAQVLATQMALYS-D-P 121

Query 126  EEVSKLA--KVKAQVSEVKGVMMENIEKVLDRGEKIELLV DKTENLRSQAQDFRQQGTNV 183
          A KV+ +V EVK VM +NIEKVL+RGE+I++L+DK E L + AQ F++ + +
Sbjct 122  GRAGGDAINKVQREVDEVKDVMTKNIEKVLGERIDILMDKAETLDNSAQTFQRHSSRL 181

Query 184  RRKMWLQNMKI 194
          R+KMW QN ++
Sbjct 182  RKKMWWQNTRM 192
```

>ref|NP\_180106.1| **UG** ATVAMP712 (Arabidopsis thaliana vesicle-associated membran 712)

sp|Q9SIQ9|VA712\_ARATH **G** Vesicle-associated membrane protein 712 (AtVAMP712)

gb|AAD23657.1| **G** putative synaptobrevin [Arabidopsis thaliana]  
Length=219

GENE ID: 817072 ATVAMP712 | ATVAMP712 (Arabidopsis thaliana vesicle-associated membrane protein 712) [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 140 bits (354), Expect = 5e-32, Method: Compositional matrix adjust.  
Identities = 75/213 (35%), Positives = 133/213 (62%), Gaps = 3/213 (1%)

```
Query 5  SLIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPAS--NNKFTYNC DGHTFNYLVEDGF 63
          S++YA VARGTV+LAE + + N +TIA Q L K+P + ++ +Y+ D + F+ DG
Sbjct 2  SILYALVARGTVVLAELSTTSTNASTIAKQILEKIPGNGDSHVSYSQDRYVFHVKRTDGL 61

Query 64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVD 123
          T +A E G++IP +F++ + + F + YG +A A ++N EF L + ++Y +
Sbjct 62  TVLCMADEDAGRRIPFSFLEDIHQRFVRTYGRA-IHSAQAYAMNDEF SRVLNQIEEYYSN 120

Query 124  HP EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLV DKTENLRSQAQDFRQQGTNV 183
          P +++++K +++++V+ VM+ENI+ +LDRGE++ELLVDKT N++ FR+Q
Sbjct 121  DPN-ADTISRIGEMNQVRDVM IENIDNILD RGERLELLVDKTANMQGNTFRFRKQTRRF 179

Query 184  RRKMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
          +W +N K+ L+++ +++ +I I + CHG
Sbjct 180  NNTVWWRNCKLTLLLLILVLLVVIYIGVAFACHG 212
```

>ref|NP\_001048427.1| **UG** Os02g0803600 [Oryza sativa (japonica cultivar-group)]

dbj|BAD36041.1| **G** putative synaptobrevin 1 [Oryza sativa Japonica Group]

dbj|BAF10341.1| **G** Os02g0803600 [Oryza sativa (japonica cultivar-group)]  
Length=226

GENE ID: 4331049 Os02g0803600 | Os02g0803600 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 137 bits (346), Expect = 4e-31, Method: Compositional matrix adjust.  
Identities = 73/217 (33%), Positives = 127/217 (58%), Gaps = 9/217 (4%)

```
Query 8  YAFVARGTVILAEYTEFT--GNFTTIIASQCLMKLPASNN-----KFTYNC DGHTFNYLVE 60
          YA VARG V++AE+ + N +A Q L +L A + +Y D H F+
Sbjct 6  YAAVARGAVVMAEHGDAAFPNAGAVARQILDRLSAGDGGGGGDCNISYTQDLHV FHVKRT 65

Query 61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DG T +A ++ G++IP AF++ + F K YG A TA A ++N EF L + M Y
```

```

Sbjct 66 DGV TALCMADDAAGRRIPFAFLEDIHGRFVKTYGRA-ALTALAYAMNDEF SRVLGQQMDY 124
Query 121 CVDHP EEVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQG 180
      + P ++++++ ++ +V+ VM++NI+KVL+RG+++ELLVDKT ++ F++Q
Sbjct 125 YSNDPN-ADRI SRMRGEMDQVRNVMIDNIDKVL ERGDRLELLVDKTATMQGNTMRFRKQA 183
Query 181 TNVRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
      R +W +N+K+ + I++ +I I+++ +CHGF
Sbjct 184 RFRNTVWWRNVKLTAASVFILLV IYIVLVYMCHGF 220

```

>ref|NP\_001086871.1| **UG** synaptobrevin-like 1 [Xenopus laevis]  
 gb|AAH77586.1| **G** Syb11-prov protein [Xenopus laevis]  
 Length=220

GENE ID: 446706 syb11 | synaptobrevin-like 1 [Xenopus laevis]  
 (10 or fewer PubMed links)

Score = 137 bits (345), Expect = 5e-31, Method: Compositional matrix adjust.  
 Identities = 71/192 (36%), Positives = 115/192 (59%), Gaps = 6/192 (3%)

```

Query 5 SLIYAFVARGTVILA EYTEFTGNFTT IASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
      ++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2 AILFAVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHG SYLFHYMCQDR II 61
Query 65 YCVVAVESVGQ QIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
      Y + + + F++ +K+ F YG +A TA ++N EF S L ++Y H
Sbjct 62 YLCITDDDFERSRAFNFLNEIKRFRQTTYGS-RAQTALPYAMNSEFSSVLSAQLKY---H 117
Query 125 PE--EVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQGTN 182
      E V ++A+ +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N
Sbjct 118 SENKSVDRAETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN 177
Query 183 VRRKMWLQNMKI 194
      + R M ++N+K+
Sbjct 178 LARAMCMKNLKL 189

```

>ref|XP\_566592.1| **G** vesicle-associated membrane protein 712 [Cryptococcus neoformans var. neoformans JEC21]  
 gb|AAW40773.1| **G** vesicle-associated membrane protein 712, putative [Cryptococcus neoformans var. neoformans JEC21]  
 Length=306

GENE ID: 3253707 CNA02090 | vesicle-associated membrane protein 712  
 [Cryptococcus neoformans var. neoformans JEC21] (10 or fewer PubMed links)

Score = 136 bits (343), Expect = 8e-31, Method: Compositional matrix adjust.  
 Identities = 73/192 (38%), Positives = 116/192 (60%), Gaps = 5/192 (2%)

```

Query 5 SLIYAFVARGTVILA EYTEFTGNFTT IAS-QCLMKLPASNNKFTYNCDGHTFNYLVEDGF 63
      SLI+A +ARGT +LAE+ T A L K+P +N+K TY +Y+ +G
Sbjct 89 SLIHALIARGTTVLA EHATGTAE LKPAQAQITILSKIPPNN SKLTYVWQDR LIHYVSSNGV 148
Query 64 TYCVVAVESVGQ QIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHM-QYCV 122
      Y V+A +SVG+++P AF+ ++ FT +Y +A A+SL EF +L + M QY
Sbjct 149 IYLVMA DSVGRMPFAFLADLERRFTAQYESDDIVSAGAH SLE-EFEPELAKLMHQYTS 207
Query 123 DHPEEVSKLAKVKAQVSEVKGVM MENIEKV LDRGEKIELLV DKTENLRSQAQDFRQQGTN 182
      P + L + ++ ++ VK +M++NI+ +L RGE+++LLVDKT+ L QA FR+ +
Sbjct 208 SPPAD--PLRQAQSDLN NVKDIMVQNIDSILQRGERLDLLVDKTD TLAGQAYAFRRGARS 265
Query 183 VRRKMWLQNMKI 194
      VRR+ W +NM+I
Sbjct 266 VRRQQWKNMRI 277

```

>ref|XP\_778199.1| **G** hypothetical protein CNBA1990 [Cryptococcus neoformans var. B-3501A]  
 gb|EAL23552.1| **G** hypothetical protein CNBA1990 [Cryptococcus neoformans var. ne B-3501A]

Length=306

GENE ID: 4933450 CNBA1990 | hypothetical protein  
[Cryptococcus neoformans var. neoformans B-3501A]

Score = 136 bits (342), Expect = 1e-30, Method: Compositional matrix adjust.  
Identities = 73/192 (38%), Positives = 116/192 (60%), Gaps = 5/192 (2%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTAS-QCLMKLPASNNKFTYNCDGHTFNYLVEDGF 63
          SLI+A +ARGT +LAE+   T   A   L K+P +N+K TY   +Y+ +G
Sbjct 89  SLIHALIARGTTVLAEHATGTAE LKPA AQITILSKIPPNNNSKLTYVWQDRLIHYVSSNGV 148

Query 64  TYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHM-QYCV 122
          Y V+A +SVG+++P AF+   ++ FT +Y   +A A+SL EF +L + M QY
Sbjct 149  IYLMADDSSVGRRMPFAFLADLERRFTAQYESDDIVSAGAHSL-EFEPELAKLMHQYTS 207

Query 123  DHPEEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTN 182
          P +   L + ++ ++ VK +M++NI+ +L RGE+++LLVDKT+ L QA FR+ +
Sbjct 208  SPPAD--PLRQAQSDLNNVKDIMVQNIDSILQ RGERLDLLVDKTD TLAGQAYAFRRGARS 265

Query 183  VRRKMWLQNMKI 194
          VRR+ W +NM+I
Sbjct 266  VRRQQWKNMRI 277

```

>ref|NP\_001026292.1| **UG** synaptobrevin-like 1 [Gallus gallus]  
 sp|Q5ZL74.1|VAMP7\_CHICK **G** Vesicle-associated membrane protein 7 (Synaptobrevin-1)  
 emb|CAG31519.1| **G** hypothetical protein [Gallus gallus]  
 Length=220

GENE ID: 422297 RCJMB04 7f19 | vesicle-associated membrane protein 7  
[Gallus gallus] (10 or fewer PubMed links)

Score = 135 bits (341), Expect = 1e-30, Method: Compositional matrix adjust.  
Identities = 71/192 (36%), Positives = 114/192 (59%), Gaps = 6/192 (3%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          ++++A VARGT ILA++   GNF + Q L K+P+ NNK TY+   + F+Y+ +D
Sbjct 2  AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRII 61

Query 65  YCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          Y + + +   F++ +K+ F   YG +A TA   ++N EF S L   ++Y H
Sbjct 62  YLCITDDDFERSRAFNFLNEIKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKY---H 117

Query 125  PEE--VSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTN 182
          E   ++A+ +AQV E+KG+M+ NI+ V RGEK+ELL+DKTENL + F+ N
Sbjct 118  SESKGTQVAETQAQVDELKGIMVRNIDLVAQRGEKLELLIDKTENLVDSSVTFKTTSRN 177

Query 183  VRRKMWLQNMKI 194
          + R M ++N+K+
Sbjct 178  LARAMCMKNLKL 189

```

>gb|ABP03854.1| Longin-like [Medicago truncatula]  
 Length=224

Score = 135 bits (340), Expect = 2e-30, Method: Compositional matrix adjust.  
Identities = 70/217 (32%), Positives = 127/217 (58%), Gaps = 9/217 (4%)

```

Query 6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKF-----TYNCDGHTFNYLVE 60
          ++Y VARG V+LAE++   N + +A Q L ++   N +   +++ D + F+
Sbjct 3  ILYGMVARGQVVLAEFSVIQSNASVVAQKILNQINQGTNSYNSNVFSHSDRYVFHVRRT 62

Query 61  DGFTYCVVAVESVGQQIPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQY 120
          DG T   +A E+ G++IP +F++ +   F K Y G   +A A ++N EF L + M Y
Sbjct 63  DGLTVLCMADEAFGRRIIPFSFLEDIHNRFVKTYAGA-ILSAPAYTMNDEF SRILSQQMDY 121

Query 121  CVDHPEEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQG 180
          P   +L ++K ++++V+ VM++NIEKVL+RG ++E+LV+KT + + + F++Q
Sbjct 122  YSTDPN-ADRLNRLKGEMTQVRTVMLDNIEKVLERGGRLEMLVEKTATMNTNSVRFKRQA 180

Query 181  TNVRRKMWLQNMKIKLIVLGIIIALILIIILS-VCHG 216

```

+ MW N+++ + L +I A++ IIL+ +CHG  
 Sbjct 181 RRYKNNMWSNVRLT-VALIMIFAIVFYIILAFMCHG 216

>ref|NP\_610524.1| **UG** CG1599 CG1599-PA [Drosophila melanogaster]  
 gb|AAF58892.1| **G** CG1599-PA [Drosophila melanogaster]  
 gb|AAL49317.1| **G** RH15778p [Drosophila melanogaster]  
 Length=218

GENE ID: 36015 CG1599 | CG1599 [Drosophila melanogaster]  
 (10 or fewer PubMed links)

Score = 135 bits (339), Expect = 2e-30, Method: Compositional matrix adjust.  
 Identities = 69/211 (32%), Positives = 124/211 (58%), Gaps = 3/211 (1%)

```

Query 6  LIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFTY 65
          ++Y+ ++RGT +LA++ E GNF + + ++ N+K TY + +Y E+ Y
Sbjct 3  ILYSVISRGTTVLAKFAECVGNFAEVTEHIIGRIGVHNHKMTYTHGDYLIHYTCENKLVY 62

Query 66 CVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP 125
          + + F+ +K+ F + YG + ATA A S+N EF L + M Y
Sbjct 63 MCITDNEFERSRAFLFLADIKQKFQTYGL-QVATAIAYSMTNTEFSKILAQQMVFY-FSQS 120

Query 126 EEVSKLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQGTNVRR 185
          EV +++V Q+ E+K +M++NI+ + DRGEK+ELLV+KTENL + + FR+ N+ R
Sbjct 121 REVDTISRVHGGQIDELKDIMVKNIDSLRDRGEKLELLVNKTENLSNNSVAFRKASRNLR 180

Query 186 KMWLQNMKIKLIVLGIILILILILSVCHG 216
          +M+ +N+++ +V+G++I I+ +I+S+ G
Sbjct 181 QMFWKNIIRV-YVVVGLVITFIVYVIVSMACG 210

```

>ref|NP\_035645.1| **UG** vesicle-associated membrane protein 7 [Mus musculus]  
 sp|P70280.1|VAMP7\_MOUSE **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synap  
 protein 1)  
 emb|CAA65509.1| **G** synaptobrevin-like protein [Mus musculus]  
 8 more sequence titles

emb|CAB94231.1| **G** synaptobrevin-like protein [Mus musculus]  
 dbj|BAB22386.1| **G** unnamed protein product [Mus musculus]  
 dbj|BAB27667.1| **G** unnamed protein product [Mus musculus]  
 gb|AAH03764.1| **G** Synaptobrevin like 1 [Mus musculus]  
 dbj|BAC40712.1| **G** unnamed protein product [Mus musculus]  
 dbj|BAE38126.1| **G** unnamed protein product [Mus musculus]  
 gb|ABK42476.1| VAMP7 [synthetic construct]  
 gb|EDL07809.1| **G** synaptobrevin like 1, isoform CRA\_c [Mus musculus]  
 Length=220

GENE ID: 20955 Vamp7 | vesicle-associated membrane protein 7 [Mus musculus]  
 (Over 10 PubMed links)

Score = 134 bits (337), Expect = 4e-30, Method: Compositional matrix adjust.  
 Identities = 71/192 (36%), Positives = 115/192 (59%), Gaps = 6/192 (3%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
          +++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2  AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 61

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          Y + + + +F++ VK+ F YG +A TA ++N EF S L +++ H
Sbjct 62 YLCITDDDFERSRAFSFLNEVKRFRQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H 117

Query 125 PEEVS--KLAKVKAQVSEVKGVMMENIEKVLDGRGEKIELLVDKTENLRSQAQDFRQQGTN 182
          E S K+ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N
Sbjct 118 SENKSLDKVMETQAQVDELKGMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN 177

Query 183 VRRKMWLQNMKI 194

```

Sbjct 178 + R M ++N+K+ LARAMCMKNIKL 189

>emb|CAH69613.1| synaptobrevin 1-2 [Paramecium tetraurelia]  
Length=228

Score = 134 bits (337), Expect = 4e-30, Method: Compositional matrix adjust.  
Identities = 71/216 (32%), Positives = 130/216 (60%), Gaps = 3/216 (1%)

```
Query 6  LIYAFVARGT-VILAEYTEFTGNFTTIIASQCLMKLPASNKFTYNCDGHTFNYLVEDGFT 64
          +IYA V RG+ V+L+EY+ GN+ A + K+ SN K ++N + + F+ LVEDGF+
Sbjct 8  IIYAVVVRGSNNVLSEYSIAKGNYIAFAKTIISKVNQSNAKKSFNYEQYEFHILVEDGFS 67

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          + ++A + +I A ++ +K+ F + + + A + LN +F + K ++Y +
Sbjct 68 FLIMAERGLKMRIAFACLEDKQKFFQMFQPPQORDQAISYGLNSQFSIEQKNKIEYY--N 125

Query 125 PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTNVR 184
          + KL V + + K VMMEN++K+L+RGEKI++LV+KT + + + ++ T +R
Sbjct 126 SPQADKLRMVSDNIQQTKEVMMENLDKLLERGEKIDILVEKTNVMVNISTSMKENATTLR 185

Query 185 RKMWLQNMKIKLIVLGIILIIILSVCHGFKCH 220
          R+MW +N+K+ +I++ + + I II++ C GF H
Sbjct 186 RQMWWRNKMTIILVLVGLLAIYIIMVIACGGFAMH 221
```

>ref|XP\_001439963.1| **G** hypothetical protein GSPATT00008957001 [Paramecium tetraurelia strain d4-2]  
emb|CAD97455.1| synaptobrevin 1 [Paramecium tetraurelia]  
emb|CAK72566.1| **G** unnamed protein product [Paramecium tetraurelia]  
Length=228

GENE ID: 5025748 GSPATT00008957001 | hypothetical protein  
[Paramecium tetraurelia strain d4-2]

Score = 134 bits (337), Expect = 4e-30, Method: Compositional matrix adjust.  
Identities = 72/216 (33%), Positives = 125/216 (57%), Gaps = 3/216 (1%)

```
Query 6  LIYAFVARGT-VILAEYTEFTGNFTTIIASQCLMKLPASNKFTYNCDGHTFNYLVEDGFT 64
          +IYA VARG+ + L+EY+ GN+ + L K+ N K ++N + + F+ LVEDGF+
Sbjct 8  IIYAVVARGSNLFLSEYSILKGNIDFSKTIILSKVNQQNAKKSFNYEQYEFHILVEDGFS 67

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
          + ++A + +I A ++ +K+ F + + + A + LN +F + K +QY +
Sbjct 68 FLIMADRGGLKMRIAFACLEDKQKFFQMFQPPQORDKAMSYGLNSQFSIEQKNQIQYY--N 125

Query 125 PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQOGTNVR 184
          + KL V + + K VMMEN++K+L+RG+KIE+LV KT+ + + R T +R
Sbjct 126 SPQADKLRMVSDNIQQTQDVMMENLDKLLERGDKIEILVVKTDQMAMLSTTMRNATTLR 185

Query 185 RKMWLQNMKIKLIVLGIILIIILSVCHGFKCH 220
          R+MW +N K+ LI++ + + I I++ C GF H
Sbjct 186 RQMWWRNKKMMLIMILVGLLAIYFIMVIACGGFAMH 221
```

>ref|XP\_795809.2| **UG** PREDICTED: similar to Syb11-prov protein [Strongylocentrotus purpuratus]

ref|XP\_001188931.1| **G** PREDICTED: similar to Syb11-prov protein [Strongylocentrotus purpuratus]  
Length=220

GENE ID: 591136 LOC591136 | similar to Syb11-prov protein  
[Strongylocentrotus purpuratus]

Score = 134 bits (336), Expect = 5e-30, Method: Compositional matrix adjust.  
Identities = 68/212 (32%), Positives = 125/212 (58%), Gaps = 1/212 (0%)

```
Query 6  LIYAFVARGTVILAEYTEFTGNFTTIIASQCLMKLPASNKFTYNCDGHTFNYLVEDGFTY 65
          ++YA +ARGT +LA Y GNFT + Q LMK+P N K TY+ + F+Y+ ++ Y
Sbjct 3  ILYAVIARGTTVLANYAACQGNFTEVTEQVLMKIPPQNAKLTYSHGAYLFHYVSDERIIY 62

Query 66 CVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDHP 125
```

```

      + + + AF+ +K+ FT YG + TA ++N EF L ++Y
Sbjct 63 MCITDDDFERSRAFAFLQEIKKKFTATYGS-RVHTALPFAMNSEFSRVLAAQIRYFAQPL 121
Query 126 EEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVRR 185
      + +++++V+ + E+ +M+ NIE V +RGE++ELL+DKTE+L + + F++ ++ R
Sbjct 122 SDHTRMSEVQQDLEELNQIMVRNIESVSNRGERLELLIDKTEDLETTSLTFKKSSKSLAR 181
Query 186 KMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
      M+++N+K+ +I+ ++I +I I+ + C G
Sbjct 182 SMFMKNLKLIILSIVVILVIYFIVSAACGGL 213

```

>dbj|BAD96514.1| **G** synaptobrevin-like 1 variant [Homo sapiens]  
Length=220

GENE ID: 6845 VAMP7 | vesicle-associated membrane protein 7 [Homo sapiens]  
(Over 10 PubMed links)

Score = 134 bits (336), Expect = 6e-30, Method: Compositional matrix adjust.  
Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
      ++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2 AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 61
Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
      Y + + + F++ +K+ F YG +A TA ++N EF S L +++ H
Sbjct 62 YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTAPPYAMNSEFSSVLAAQLKH---H 117
Query 125 PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN 182
      E + K+ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N
Sbjct 118 SENKGLDKVMETQAQVDELKGMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN 177
Query 183 VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
      + R M ++N+K+ +I++ + I I II+ +C GF
Sbjct 178 LARAMCMKNLKLTIIIIIIVSIVFIYIIIVSPLCGGF 212

```

>ref|NP\_005629.1| **UG** vesicle-associated membrane protein 7 [Homo sapiens]  
ref|XP\_001100334.1| **UG** PREDICTED: synaptobrevin-like 1 isoform 3 [Macaca mulatta]  
ref|XP\_001498248.1| **UG** PREDICTED: similar to ORF isoform 1 [Equus caballus]  
6 more sequence titles

sp|P51809.3|VAMP7\_HUMAN **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-1) (Tetanus-insensitive VAMP) (Ti-VAMP)

emb|CAA63133.1| **G** ORF [Homo sapiens]

emb|CAB96816.1| **G** synaptobrevin-like 1 protein [Homo sapiens]

gb|AAH56141.1| **G** Vesicle-associated membrane protein 7 [Homo sapiens]

gb|EAW55882.1| **G** synaptobrevin-like 1, isoform CRA\_e [Homo sapiens]

gb|EAW55883.1| **G** synaptobrevin-like 1, isoform CRA\_e [Homo sapiens]

Length=220

GENE ID: 6845 VAMP7 | vesicle-associated membrane protein 7 [Homo sapiens]  
(Over 10 PubMed links)

Score = 133 bits (335), Expect = 8e-30, Method: Compositional matrix adjust.  
Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

```

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64
      ++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2 AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 61
Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
      Y + + + F++ +K+ F YG +A TA ++N EF S L +++ H
Sbjct 62 YLCITDDDFERSRAFNFLNEIKKRFQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H 117
Query 125 PEE--VSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTN 182
      E + K+ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N
Sbjct 118 SENKGLDKVMETQAQVDELKGMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN 177

```

Query 183 VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217  
 + R M ++N+K+ +I++ + I I II+ +C GF  
 Sbjct 178 LARAMCMKNLKLTIIIIIIVSIVFIYIIIVSPLCGGF 212

>ref|XP\_855489.1| **UG** PREDICTED: similar to Synaptobrevin-like protein 1 [Canis  
 Length=331

GENE ID: 612663 VAMP7 | vesicle-associated membrane protein 7  
 [Canis lupus familiaris]

Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.  
 Identities = 75/213 (35%), Positives = 129/213 (60%), Gaps = 2/213 (0%)

Query 5 SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64  
 +++A VARGT ILA++ GN+ + Q L K+P+ NNK TY+ + F+Y+ +D  
 Sbjct 113 AILFAVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 172

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124  
 Y + + + F++ +K+ F YG +A TA ++N EF S L +++ ++  
 Sbjct 173 YLCITDDDFERSRAFNFLNEIKRFRQTTYGS-RAQTALPYAMNSEFSSVLAAQLKHSEN 231

Query 125 PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR 184  
 + + K+ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N+  
 Sbjct 232 -KGIDKVVETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSTFKTTSRNL 290

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217  
 R M ++N+K+ +I++ + I I II+ +C GF  
 Sbjct 291 RAMCMKNLKLTIIIIIIVSIVFIYIIIVSPLCGGF 323

>ref|XP\_001459953.1| **UG** hypothetical protein GSPATT00025290001 [Paramecium tetr  
 strain d4-2]

emb|CAK92556.1| **G** unnamed protein product [Paramecium tetraurelia]  
 Length=228

GENE ID: 5045738 GSPATT00025290001 | hypothetical protein  
 [Paramecium tetraurelia strain d4-2]

Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.  
 Identities = 71/216 (32%), Positives = 129/216 (59%), Gaps = 3/216 (1%)

Query 6 LIYAFVARGT-VILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDGHTFNYLVEDGFT 64  
 +IYA V RG+ V+L+EY+ GN+ A + K+ SN K ++N + + F+ LVEDGF+  
 Sbjct 8 IYAVVVRGSNVVLSEYSIAKGNYIAFAKTIISKVNQSNKKSFNIEQYEFHILVEDGFS 67

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124  
 + ++A + +I A ++ +K+ F + + + A + LN +F + K ++Y +  
 Sbjct 68 FLIMAERGLKMRIAFACLEDMDKQKFFQMFQPPQORDQAISYGLNSQFSIEQKNKIEYY--N 125

Query 125 PEEVSKLAKVKAQVSEVKGVMMENIEKVLDRGEKIELLVDKTENLRSQAQDFRQQGTNVR 184  
 + KL V + + K VMMEN++K+L+RGEKI++LV+KT + + + ++ T +R  
 Sbjct 126 SPQADKLRMVSDNIQQTKEVMMENLDKLLERGEKIDILVEKTNVMVNISTSMKENATTLR 185

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGFKCH 220  
 R+MW +N K+ +I++ + + I II++ C GF H  
 Sbjct 186 RQMWWRNKKMTIILVLVGLLAIYIIMVIACGGFAMH 221

>ref|NP\_445983.1| **UG** vesicle-associated membrane protein 7 [Rattus norvegicus]  
 sp|Q9JHW5.1|VAMP7\_RAT **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synapto  
 protein 1)

gb|AAF88059.1|AF281632\_1 **G** vesicle-associated membrane protein 7 [Rattus norveg  
 gb|EDL83883.1| **G** synaptobrevin-like 1, isoform CRA\_b [Rattus norvegicus]  
 Length=220

GENE ID: 85491 Syb11 | synaptobrevin-like 1 [Rattus norvegicus]  
 (10 or fewer PubMed links)

Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.

Identities = 75/213 (35%), Positives = 128/213 (60%), Gaps = 2/213 (0%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVEDGFT 64
++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2  AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 61

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
Y + + + F++ VK+ F YG +A TA ++N EF S L +++ ++
Sbjct 62 YLCITDDDFERSRAFGFLNEVKRFRQTTYGS-RAQTALPYAMNSEFSSVLAAQLKHSEN 120

Query 125 PEEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTNVR 184
+ + ++ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N+
Sbjct 121 -QSLDRV TETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRNLA 179

Query 185 RKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
R M ++N+K+ I++ + I I II+ +C GF
Sbjct 180 RAMCVKNVKLTAIIVVVSIVFIYIIIVSPLCGGF 212

```

>ref|NP\_001069770.1| **UG** vesicle-associated membrane protein 7 [Bos taurus]  
 sp|Q17QI5.1|VAMP7\_BOVIN **G** Vesicle-associated membrane protein 7 (VAMP-7) (Synap  
 protein 1)  
 gb|AAI18342.1| **G** Similar to Synaptobrevin-like protein 1 [Bos taurus]  
 Length=220

GENE ID: 613984 SYBL1 | vesicle-associated membrane protein 7 [Bos taurus]

Score = 133 bits (334), Expect = 9e-30, Method: Compositional matrix adjust.  
 Identities = 77/215 (35%), Positives = 128/215 (59%), Gaps = 6/215 (2%)

```

Query 5  SLIYAFVARGTVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNC DGHTFNYLVEDGFT 64
++++A VARGT ILA++ GNF + Q L K+P+ NNK TY+ + F+Y+ +D
Sbjct 2  AILFAVVARGTTILAKHAWCGGNFLEVTEQILAKIPSENNKLTYSHGNYLFHYICQDRIV 61

Query 65 YCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATAAANSLNREFGSKLKEHMQYCVDH 124
Y + + + F++ +K+ F YG +A TA ++N EF S L +++ H
Sbjct 62 YLCITDDDFERSRAFNFLNEIKRFRQTTYGS-RAQTALPYAMNSEFSSVLAAQLKH---H 117

Query 125 PEE--VSKLAKVKAQVSEVKGVMENIEKVLD RGEKIELLV DKTENLRSQAQDFRQQGTN 182
E + K+ + +AQV E+KG+M+ NI+ V RGE++ELL+DKTENL + F+ N
Sbjct 118 SENKGLDKVMETQAQVDELKGIMVRNIDLVAQRGERLELLIDKTENLVDSSVTFKTTSRN 177

Query 183 VRRKMWLQNMKIKLIVLGIIIALILIIILSVCHGF 217
+ R M ++N+K+ +I++ I + I II+ +C GF
Sbjct 178 LARAMCMKNLKLTIIIIIISVVFYIIIVSPLCGGF 212

```

>dbj|BAE99604.1| synaptobrevin-like protein [Arabidopsis thaliana]  
 Length=186

Score = 133 bits (334), Expect = 1e-29, Method: Compositional matrix adjust.  
 Identities = 62/175 (35%), Positives = 112/175 (64%), Gaps = 2/175 (1%)

```

Query 42 SNNKFTYNC DGHTFNYLVEDGFTYCVVAVESVGQIQPIAFMDRVKEDFTKRYGGGKAATA 101
S+ + ++ D + F+ L DG T+ +A ++ G+++P +++++ + F K YG A A
Sbjct 6  SDERLCFSQDRYIFHILRS DGLTFLCMANDTFGRVPF SYLEEIHMRFMKNYK-VAHNA 64

Query 102 AANSLNREFGSKLKEHMQYCVDHP EEVSKLAKVKAQVSEVKGVMENIEKVLD RGEKIEL 161
A ++N EF L + M++ +P V L +V+ +VSE++ VM+ENIEK+++RG++IEL
Sbjct 65 PAYAMNDEF SRVLHQQMEFFSSNPS-VDTLNRVRGEVSEIRSV MVENIEKIMERGDRIEL 123

Query 162 LVDKTENLRSQAQDFRQQGTNRRKMWLQNMKIKLIVLGIIIALILIIILSVCHG 216
LVDKT ++ + FR+Q +RR +W++N K+ +++ +I+ L+ III S C G
Sbjct 124 LVDKTATMQDSSFHFRKQSKRLRRALWMKNAKLLVLLTCLIVFLLYIIIIASF CGG 178

```

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